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Novel regulators of human gonadal development



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Declaration

The studies undertaken in the thesis were the sole work of the author, except where acknowledgement is made by reference. The work described in this thesis has not been previously accepted for, or is currently being submitted for another degree or qualification at the University of Edinburgh or any other institution.

Sharon Eddie

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Abstract

The production of viable germ cells during human embryonic development determines adult reproductive success. This is particularly true for females, as development of germ cells (GCs) into primordial follicles before birth is imperative for future fertility. During fetal development GCs migrate to the genital ridge to form the gonad, after which several tightly regulated events, including proliferation, differentiation, and association with somatic cells, must occur to form a functional gonad. In the ovary these processes also include the initiation and subsequent arrest of meiosis. These developmental processes are orchestrated by local autocrine and paracrine factors, many of which remain to be identified in the human.

In order to decipher further the pathways by which the gonad and GCs develop, potential regulators including prostaglandin (PG) E₂, the interleukin (IL)6-type cytokines, and the prokinetecins (PROKs), were examined in the human fetal ovary and PROKs in the human fetal testis. Patterns of gene expression, protein localisation, function, and interaction of the potential mediators throughout human development (8-20 weeks gestation) were determined. Primary fetal tissue was investigated, in addition to immortalized GCs (T-Cam2 cells) and a murine model of fetal ovarian development.

PGE₂ interacts with known regulators of GC development in non-reproductive organs. It was postulated PGE₂ may regulate GC progression by modulating these factors. Examination of PGE₂ receptors and precursor enzymes in the fetal ovary revealed that all were present and some were developmentally regulated, with mRNA expression increasing with gestation. These developmentally regulated components were localised to the GCs. The PGE₂ receptors were among those differentially expressed, with one localised solely to mature GCs. Culture of human fetal ovary confirmed that PGE₂ regulates known regulators of GC development, increasing expression of survival and anti-apoptotic factors. To test the hypothesis that PGE₂ is necessary for female GC development, paracetamol, an inhibitor of PGE₂ precursor enzymes, was utilised in a murine model of fetal exposure. Fetal ovaries from this experiment displayed disruption of normal development.

The IL6-type cytokines are also postulated to be involved in early gonad development, and are known to regulate proliferation and differentiation of mouse embryonic stem and GCs *in vitro*. A significant increase in transcript levels of the shared receptor components was determined in second trimester human ovaries, as well as developmental increases of several of the IL6-type ligands. Both common receptor components were located specifically in the GCs identifying them as the target of IL6 action in the human fetal ovary.

The PROKs regulate cell migration, proliferation and differentiation, and modulate secretion of PGE₂ and expression of some IL6-type cytokines. To-date, PROKs have not been examined in the human fetal gonad. Transcript levels were higher in the fetal testis compared to the ovary, with receptor and ligand components increasing with gestation. Most components also increased with gestation in the ovary.

However, location of PROK components was strikingly different between the two tissues, with GCs being the primary target of PROK action in the fetal ovary, and Leydig and interstitial cells being the target in the testis. PROKs interaction with other regulators of gonad development was examined utilising a GC line in the case of the ovary and primary interstitial cell cultures in the case of the testis.

These studies have identified new factors involved in human fetal gonad development, and how they interact with known regulatory pathways of development.

Presentations relating to this thesis

Oral Presentations

Prokineticins Exert Anti-Apoptotic Effects in the Human Fetal Testis
Society for the Study of Reproduction Portland, OR, USA 2011

Identifying the Targets of IL-6 Ligand Action in the Human Fetal Ovary
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Poster Presentations

Maternal Paracetamol Administration Affects Fetal Ovarian Germ Cell Development
Society for Reproduction and Fertility Brighton, UK 2011

Maternal Acetaminaphen Affects on Fetal Ovarian Germ Cell Development
Society for Gynecological Investigation Miami, FL, USA 2011

Prokineticins in the Human Fetal Testis
Society for Reproduction and Fertility Nottingham, UK 2010

Prokineticins in the Human Fetal Ovary
National Ovarian Workshop Cambridge, UK 2009

Novel Effects of Prostaglandin E2 in the Developing Human Ovary
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Publications relating to this thesis

Bayne R, **Eddie S**, *et al.* Prostaglandin E2 as a regulator of germ cells during ovarian development. *JCEM* **2009** 10:4053-60.

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Full text can be found in the appendices.

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Commonly Used Abbreviations

AMH	anti-Müllerian hormone	NS	normal serum
BAD	BCL-2 associated agonist of cell death	NSAID	non-steroidal anti-inflammatory drug
BAX	BCL-2 associate X protein	NT4	neurotrophin-4
BCL-2	B-cell lymphoma/leukemia-2	OSM	oncostatin-M
BDNF	brain-derived neurotrophic factor	OSMR	oncostatin-M receptor
bFGF	basic fibroblast growth factor	PBS	phosphate buffered saline
BMP	bone morphogenic protein	PG	pre-granulosa cell
bp	base pair	PGC	primordial germ cell
BrdU	5-bromo-2'-deoxyuridine	PHH3	phospho-histone H3
BSA	bovine serum albumin	pnd	postnatal day
C°	degrees Celsius	POI	premature ovarian insufficiency
CC3	cleaved caspase-3	PROK	prokineticin
cDNA	Complementary Deoxyribonucleic Acid	PROKR	prokineticin receptor
c-Kit	Kit ligand receptor	PTGES	prostaglandin E synthase
CNTF	ciliary neurotrophic factor	RA	retinoic acid
CNTFR	ciliary neurotrophic factor receptor	RAR	retinoic acid receptor
COX	cyclooxygenase	rpm	revolutions per minute
CXCR4	chemokine receptor 4	RSPO1	roof plate-specific spondin-1
Dazl	deleted in azoospermia like	SDF1	stromal derived factor 1
DKK1	dickkopf homolog 1	sec	second
e	embryonic day	SF1	steroidogenic factor 1
ECM	extracellular matrix	SM	somatic cell
EP	PGE2 receptor	Socs	suppressor of cytokine signaling
ER	estrogen receptor		
ES	embryonic stem (cell)	SOHLH	spermatogenesis and oogenesis
FIGLA	factor in the germline alpha		specific basic helix-loop-helix
FOXL2	forkhead box L2	Stat	signal transducer and activator of
FOXO3a	forkhead box O3a		transcription
GC	germ cell	Stra8	stimulated by retinoic acid
GDF9	growth differentiation factor 9	TBS	tris buffered saline
GFP	green fluorescent protein	TGFβ	transforming growth factor β
gp130	glycoprotein-130		tissue non-specific alkaline
H ₂ O	water	TNAP	phosphatase
HRP	horse radish peroxidase	TRK	tropomyosin-related kinase
ID	inhibitor of differentiation	VEGF	vascular endothelial growth factor
IL6	interleukin 6		wingless-type MMTV integration site
IL6R	interleukin 6 receptor	WNT4	4
Jak	Janus kinases	wpf	weeks post fertilisation
KL	Kit ligand		
l	liter		
LHX8	LIM homeobox 8		
LIF	leukemia inhibitory factor		
LIFR	leukemia inhibitory factor receptor		
MAPK	Mitogen-Activated Protein Kinase		
Mcl-1	myeloid leukemia sequence-1		
min	minute		
MIS	Müllerian inhibiting substance		
MOF	multiple oocyte follicle		
MVH	mouse VASA homologue		
Nobox	newborn ovary homeobox		

Chapter 1

Literature Review

Chapter 1. Literature Review

1.1 Introduction

Fetal ovarian development is comprised of many complex processes, initiating with germ cell specification and migration to form the bi-potential gonad, followed by sex determination and entry to meiosis, culminating in primordial follicle formation (Edson *et al*, 2009). Proper development of the ovary and primordial follicles during fetal life will define a female's future reproductive capacity (McGee & Hsueh, 2000; Adhikari & Liu, 2010; Reddy *et al*, 2010).

Fetal ovarian development is regulated by the germ cell niche; a milieu of autocrine, juxtacrine and paracrine factors of both germ cell and somatic cell origin that govern the processes necessary for fetal ovarian function. The germ cell niche is not only important for regulation of the ovarian processes described above, but also oocyte survival and proliferation, in concert with germ cell atresia. In the human fetal ovary, germ cell numbers reach 7 million at 20 weeks (Baker, 1963), followed by rapid depletion of the oocyte population via apoptosis, such that ~85% of oocytes are lost by birth and over 99% by puberty (Baker, 1963; Forabosco *et al*, 1991) (Figure 1.1). This dynamic interplay between survival and apoptosis regulates which oocytes are available for future ovulation, disruption of which can lead to premature ovarian insufficiency (POI) or infertility.

Although some factors have been identified as regulators of these processes, their interaction with other regulators and the overall mechanisms governing fetal ovarian development remain unclear. For this reason, examination of the established factors involved in fetal ovarian development, and their interactions with possible novel mediators is essential for further understanding of this critical developmental window.

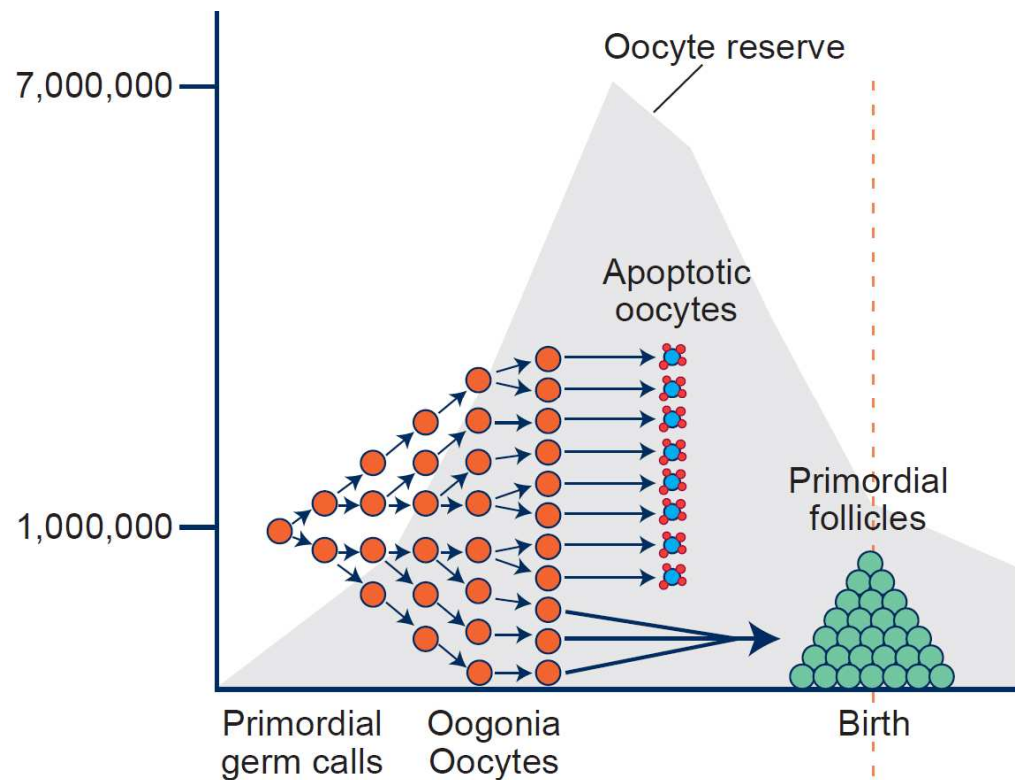


Figure 1.1 Schematic of human ovarian development.

Demonstrating germ cell number changes before birth leading up to follicle formation.

Figure adapted from (Kaipia & Hsueh, 1997).

1.2 Fetal Gonad Development

The following sections will focus predominantly on human data; however due to limitations in availability and age range of human fetal tissue, most factors are initially examined in murine models before being characterised in human tissue. Therefore, key processes and known regulators of early ovarian development will be discussed as characterised in the mouse with further more limited information in the human fetal ovary. In addition, although mouse ovarian development and primordial follicle formation involves similar processes to those in the human, there are key species-specific differences. Notably, mouse gestation is ~20 days, with primordial follicle formation occurring postnatally and nest breakdown being governed by estrogen, whereas human primordial follicle formation happens prenatally and

steroidogenic cues have not been identified-although it remains possible that they contribute. Table 1.1 summarises the key stages of ovarian development and their timing in both species.

Estimation of gestational age is done in one of two ways in the human; it is either estimated as weeks post fertilisation (wpf) or gestational age as determined from the last menstrual period (gestation) (Lynch & Zhang, 2007). Fertilisation generally occurs 2 weeks after the last menstrual period in a women with a regular 28 day cycle, thus development deemed gestational age is 2 weeks later than wpf age.

Table 1.1 Gestational comparison of ovarian development between the human and mouse

(Abbreviations: e, embryonic day; pnd, postnatal day; wpf, weeks post fertilization)

Event	Human	Human Reference	Mouse	Mouse Reference
GC Specification	≤3 w gestation	(Falin, 1969)	e 5.5	(Saitou, 2009)
GC Migration	4-5 w gestation	(Fujimoto <i>et al</i> , 1977)	e 7.5	(Anderson <i>et al</i> , 2000)
Colonisation of the Gonad	4 wpf (6 w gestation)	(Francavilla <i>et al</i> , 1990)	e10.5	(Molyneaux <i>et al</i> , 2001)
Sex Determination	6-7 wpf (8-9 w gestation)	(Moore, 1967)	e 12.5	(Adams & McLaren, 2002)
Initiation of Meiosis	11 w gestation	(Motta <i>et al</i> , 1997)	e 13.5	(Hilscher <i>et al</i> , 1974)
Primordial Follicle Formation	18 w gestation	(Hertig & Adams, 1967)	pnd 0	(Epifano & Dean, 2002)
Length of Gestation	40 w gestation	(Guerrero & Florez, 1969)	20-21 d	(Lanman & Seidman, 1977)

1.2.1 Germ Cell Specification

During mammalian fetal development, precursor cells which will develop into primordial germ cells (PGCs) originate in the proximal epiblast (Chiquoine, 1954a; Lawson & Hage, 1994), and are induced by signals from the adjacent stroma to become the germline, a process which is deemed epigenesis and occurs between embryonic days (e)5.5-7.5 in the mouse (Saitou, 2009).

Key to initiation of PGC specification is signalling from the bone morphogenic proteins (Bmp) 2, 4, and 8. Bmp4 and 8b signal from the extra embryonic ectoderm (Lawson *et al*, 1999; Ying *et al*, 2000) whereas Bmp2 signals from the visceral endoderm (Ying & Zhao, 2001). These factors signal to the proximal epiblast via their transducer proteins Smad1 and 5 which are translocated to the cell nucleus via the mediator protein Smad4 in order to interact with other transcriptional activators and modulate gene expression. Bmp signalling promotes expression of further PGC factors, which as a whole interact to suppress somatic genes and initiate the PGC pathway in a subset of cells at ~e5.5 in the mouse (Lawson *et al*, 1999). The importance of Bmp signalling was confirmed with targeted disruption of *Bmp4* and *Bmp8* in rodent models: these have a reduced number of PGCs which are unable to migrate or proliferate as a result of disruption of specification (Lawson *et al*, 1999; Ying *et al*, 2000). Mouse models with disruptions of *Smad1* or *5* also display reduced numbers of PGCs (Chang & Matzuk, 2001; Tremblay *et al*, 2001), as does disruption of their intracellular mediator *Smad4* (Chu *et al*, 2004).

Bmp signalling in precursor PGCs promotes expression of several PGC factors, most notably; interferon-inducible gene 3 (*Ifitm3/fragilis*), PR domain-containing 1 (*Prdm1/Blimp1*), and POU domain 5f1 (*Pou5f1/Oct4*) (Ying & Zhao, 2001; Saitou *et al*, 2002; Tanaka & Matsui, 2002; Ohinata *et al*, 2005; Vincent *et al*, 2005; Okamura *et al*, 2008). Bmp4 expression up-regulates *fragilis*, which was hypothesised to be key for PGC specification, as cells expressing *fragilis* at high levels initiate expression the PGC marker *Stella* and repress somatic genes such as *Hoxa1*, *Hoxb1*, *Lim1* and *Evx1* (Saitou *et al*, 2002). However, expression of *fragilis* does not confine a cell to the PGC fate pathway (Saitou *et al*, 2002; Tanaka & Matsui, 2002) and deletion of *fragilis* from embryos does not result in a phenotype

(Lange *et al*, 2008). Further, four other related genes (*fragilis2-5*) have been identified, of which *fragilis2* and *3* are also implicated in PGC specification (Saitou *et al*, 2003).

Bmp signalling also regulates *Blimp1*, a post-transcriptional repressor which functions in precursor PGCs to suppress somatic gene expression (Ohinata *et al*, 2005; Yabuta *et al*, 2006; Hayashi *et al*, 2007). *Blimp1* expression commits the fate of a cell, and is therefore thought to be the earliest PGC-specific marker (Ohinata *et al*, 2005). Along with repression of somatic genes, *Blimp1* also promotes maintenance and/or resumption of pluripotency associated genes, such as *Sox2* and *Nanog* (Ohinata *et al*, 2005; Yamaguchi *et al*, 2005; Yabuta *et al*, 2006). This role was confirmed by deletion of *Blimp1* *in vitro*, which resulted in lack of somatic gene repression, as well as only 50% of PGC-related gene induction (Saitou *et al*, 2005). Further, systemic deletion of *Blimp1* in mouse embryos resulted in a small cohort of PGC-like cells which were unable to migrate or proliferate (Ohinata *et al*, 2005; Robertson *et al*, 2007). *Prdm14*, a *Blimp1* related factor, has also recently been deemed essential for PGC specification (Yabuta *et al*, 2006; Yamaji *et al*, 2008). In addition to the pluripotency- associated factors up-regulated by *Blimp1*, *Oct4* expression is maintained in cells destined to become the germline; becoming restricted solely to these cells by e7.5 in the mouse (Scholer *et al*, 1990; Ohmura *et al*, 2004) and is also essential for PGC specification (Okamura *et al*, 2008).

1.2.2 Primordial Germ Cell Migration

Once PGCs have been specified they begin their journey to the genital ridge to form the gonad. This process is well documented in the mouse, with PGC migration initiating in the primitive streak at e7.5 (Clark & Eddy, 1975; Anderson *et al*, 2000), after which the PGCs move through the hindgut at e8.0-9.5, and arrive at the genital ridge at e10.5-e11.5 (Lawson & Hage, 1994; Molyneaux *et al*, 2001). In the human migration occurs at 4-5 week gestation (Fujimoto *et al.*, 1977). Migration is controlled by several factors including chemoattractants, guiding the cells, and regulators, initiating expression of motility factors within the PGC population. Early studies hypothesised that PGCs responded to a signal or trigger that initiated migration (Godin *et al*, 1990) and change in morphology of the PGCs prior to

initiation of migration was noted, with the cells becoming polar with cytoplasmic protrusions allowing for motility (Anderson *et al*, 2000). It is thought this trigger might be expression of Kit ligand (KL/Scf), a somatic cue necessary for PGC motility (Runyan *et al*, 2006; Gu *et al*, 2009), which functions via a tyrosine kinase receptor, c-kit, located on the PGCs themselves to promote migratory competence. Absence of KL results in a dramatic decrease of PGC migration (Godin *et al*, 1991; Manova *et al*, 1990). Bmp proteins are thought to regulate KL expression, as inhibition of Bmp signalling by the antagonist Noggin results in decreased KL expression and disruption of migration (Dudley *et al*, 2007).

Stromal derived factor 1 (Sdf1/Cxcl12) is a chemoattractant expressed by the genital ridge, which signals through the chemokine receptor 4 (Cxcr4) expressed by PGCs and is thought to guide the PGCs to the gonad (Ara *et al*, 2003; Molyneaux *et al*, 2003b; Stebler *et al*, 2004). Targeted disruption of *Cxcr4* results in a failure of PGC migration (Molyneaux *et al*, 2003b). The PGCs also utilise several components of the extracellular matrix (ECM) to aid progression of migration toward the gonad including collagen III-V, fibronectin, and laminin (Ffrenchconstant *et al*, 1991; GarciaCastro *et al*, 1997; Anderson *et al*, 1999; Soto-Suazo *et al*, 2004), all of which PGCs are able to adhere to, suggesting the ECM aids in progression of the cells. It has been suggested the ECM may be involved in concentrating other growth factors which directly regulate PGC migration (Bendel-Stenzel *et al*, 1998).

Finally, it is further postulated that cell-cell interaction is able to promote migration and survival of the PGCs. Linkage of PGCs to form a network during migration has been noted in the fetal mouse (Gomperts *et al*, 1994; Molyneaux *et al*, 2001). This hypothesis is supported by the expression of e-cadherin, Pecam1, and β 1-integrin by PGCs during migration, which are factors necessary for cell-cell adhesion and interaction (Bendel-Stenzel *et al*, 1998; Anderson *et al*, 1999; Di Carlo & De Felici, 2000; Wakayama *et al*, 2003). This may promote not only interaction with adjacent PGCs but also the surrounding stromal cells.

In addition to promotion of motility and guidance of the PGCs, several factors have been implicated in survival of the PGC cohort during migration including nanos homolog 3 (Nanos3) and dead end homolog 1 (Dnd1) (Tsuda *et al*, 2003; Youngren *et al*, 2005; Suzuki *et al*, 2009).

1.2.3 Proliferation and Colonisation of the Gonad

PGCs proliferation occurs during migration and continues upon arrival to the gonad, such that germ cells number between ~10,000-25,000 at 6 wpf in the human (8 weeks gestation) (Monk & McLaren, 1981; Byskov, 1986; Lawson & Hage, 1994; Bendtsen *et al*, 2006). This proliferation is regulated by several factors implicated in migration including KL (Dolci *et al*, 1991; Buehr *et al*, 1993; Pesce *et al*, 1993a) and SDF1, but also by the fibroblast growth factors (FGFs) (Resnick *et al*, 1992; Kawase *et al*, 2004) and possibly the interleukin-6 (IL6)-type cytokines (Defelici & Dolci, 1991; Matsui *et al*, 1991; Pesce *et al*, 1993a) which will be further discussed later in this chapter.

Upon arrival in the gonad the PGCs lose their ability to migrate (Defelici *et al*, 1992; Gomperts *et al*, 1994; GarciaCastro *et al*, 1997) and their morphology changes to a larger, rounded profile (Donovan *et al*, 1986). In addition, the PGCs lose expression of several pluripotency-associated genes (Chiquoine, 1954b; Tsuda *et al*, 2003) and genome-wide demethylation occurs (Lopes *et al*, 2008). However, expression of some pluripotency-associated genes is maintained, including *Oct4* (Scholer *et al*, 1990), but this may be because Oct4 is necessary for later function in germ cell development (Kehler *et al*, 2004). In contrast, developing germ cells begin to express a new set of gene markers including deleted in azoospermia like (Dazl) (Selgman and Page) and mouse-vasa homologue (Mvh/VASA) (Toyooka *et al*, 2000). This change in expression of germ cell markers is also observed in human fetal ovaries (Anderson *et al*, 2007), although the change in expression of OCT4 to VASA or DAZL occurs later in ovarian development in the human.

1.2.4 Sex Determination

Following germ cell migration, the gonad remains bipotential with little initial organisation of the somatic, interstitial or germ cells (Figure 1.2, page 8). In the human the process of sex determination is initiated by expression of the sex-determining region-Y (*SRY*) gene positioned on the Y chromosome in male offspring at ~6-7 weeks gestation (Gubbay *et al*, 1990; Sinclair *et al*, 1990; Tilmann & Capel, 1999; Tilmann & Capel, 2002). If an embryo has inherited a Y chromosome from the paternal donor, the *SRY* gene it carries prompts a signalling cascade resulting in a male phenotype including testis and secondary sex organs including Wolffian ducts and penis. Proof that the *SRY* gene is critical for sex determination was provided by Koopman *et al*, who demonstrated that a male phenotype results if the *SRY* gene is expressed in embryonic XX fetuses (Koopman *et al*, 1991).

SRY expression in Sertoli precursor cells triggers sex determination, although the exact mechanism by which this happens has yet to be fully elucidated (Albrecht & Eicher, 2001; Wilhelm *et al*, 2005). *SRY* prompts expression of downstream transcription factors and cytokines which induce testis formation. More specifically, *SRY* is likely to promote the up-regulation of a chemoattractant that allows for the mesonephric cells to enter the testis for the formation of seminiferous tubules (Capel *et al*, 1999).

Some of *SRY*'s downstream targets have been identified. Of known importance are the genes *SOX9* and steroidogenic factor-1 (*SF1*) (Ramkisson & Goodfellow, 1996). *SOX9* is expressed slightly after *SRY* in XY gonads (Koopman *et al*, 2001; Kobayashi *et al*, 2005), and is therefore likely to be downstream of *SRY*. It is thought the increase in *SOX9* expression is via direct regulation of a *SOX9* enhancer by *SRY* (Sekido & Lovell-Badge, 2008). However, XX genotypes expressing an additional copy of the *SOX9* gene develop testes; expression of *SOX9* alone can promote a male phenotype without the expression of *SRY* (Huang *et al*, 1999). *SOX9* and *SF1* promote masculinisation of the Sertoli and Leydig cells in the testis, thereby promoting the expression of Anti-Müllerian hormone (AMH, also known as Müllerian inhibiting substance (MIS)) and testosterone, preventing the development

of the Müllerian ducts and promoting the formation of seminiferous tubules respectively (Shen *et al*, 1994; Arango *et al*, 1999).

Until recently it was considered that the female/ovarian fate pathway was a ‘default’ based upon Alfred Jost’s experiments in the late 1940s (Jost, 1947). He noted that regardless of chromosomal sex (XX or XY), castrated fetal rabbits would develop female secondary sex organs (Wolffian ducts and external genitalia). However, the idea of a ‘default setting’ is becoming less favoured, with the consensus shifting towards the hypothesis that active signalling is necessary for both testis and ovarian development (Yao *et al*, 2002).

Starting as early as the 1980s several factors have been identified as opposing forces to the male SRY signalling pathway. This derives from the finding that XY individuals expressing two copies of an active gene on the X chromosome developed ovarian structures (Bernstein *et al*, 1980; Bardoni *et al*, 1994). This gene was identified as dosage-sensitive sex reversal-congenital adrenal hypoplasia critical region on the X chromosome protein-1 (*DAX1*) and appears to work in an antagonistic fashion against the male pathway by limiting *SF1* expression (Nachtigal *et al*, 1998; Swain *et al*, 1998). Additionally, the wingless-type MMTV integration site 4 (*Wnt4*) gene has been proven to be essential for ovarian development. Female mice homozygous null for *Wnt4* fail to form ovaries, and the structures that do form express AMH and testosterone production enzymes (Vainio *et al*, 1999). Moreover, *Wnt4*^{-/-} mice have demonstrated the protein is able to regulate follistatin expression to inhibit the formation of the male coelomic vessel (Yao *et al*, 2004).

WNT4 signals via canonical β -catenin signalling, along with another ovarian regulating factor, roof plate-specific spondin 1 (*RSPO1*; (Tevosian & Manuylov, 2008). *Rspo1*-null XX gonads are partially sex reversed (Chassot *et al*, 2008; Tomizuka *et al*, 2008), as are human female patients with mutations in the *RSPO1* gene (Parma *et al*, 2006). *Rspo1* may be up-stream or regulate *Wnt4*, as up-regulation of *Wnt4* during early ovarian development is not seen in *Rspo1*-null mice (Chassot *et al*, 2008; Tomizuka *et al*, 2008). *Wnt4* expression is down-regulated after the onset of SRY expression in the testes, denoting there is indirect regulation

of WNT4 by SRY, further promoting the male pathway (Bernard *et al*, 2008). Part of this down-regulation is due to the expression of Dickkopf homolog 1 (*DKK1*) (Manuylov *et al*, 2008), as this factor has been shown to repress Wnt4/Rspo1 β -catenin signalling (Manuylov *et al*, 2008) and is up-regulated specifically in the testes (Combes *et al*, 2011).

Another factor known to be essential for ovarian development is forkhead box L2 protein (FOXL2), as it is capable of repressing expression of *SOX9* and its downstream pathway (Ottolenghi *et al*, 2005; Wilhelm *et al*, 2009). Over-expression of FOXL2 in XY individuals results in disrupted testicular formation and mass disorganisation (deemed ovo-testes) (Ottolenghi *et al*, 2007). FOX factors are also able to interact with estrogen receptor genes (ESRs) (Carroll *et al*, 2005), which are actively involved in gonad development in other species (Crisponi *et al*, 2001; Cocquet *et al*, 2002a; Loffler *et al*, 2003) and have recently been characterised in the human fetal ovary (Fowler *et al*, 2011).

With these mediators in mind (summarised in Figure 1.2), it can be stated that ovarian development is not a default as suggested previously, but rather both testes and ovaries require active signalling for functional gonad development, as well as the ability to repress the alternative developmental pathway.

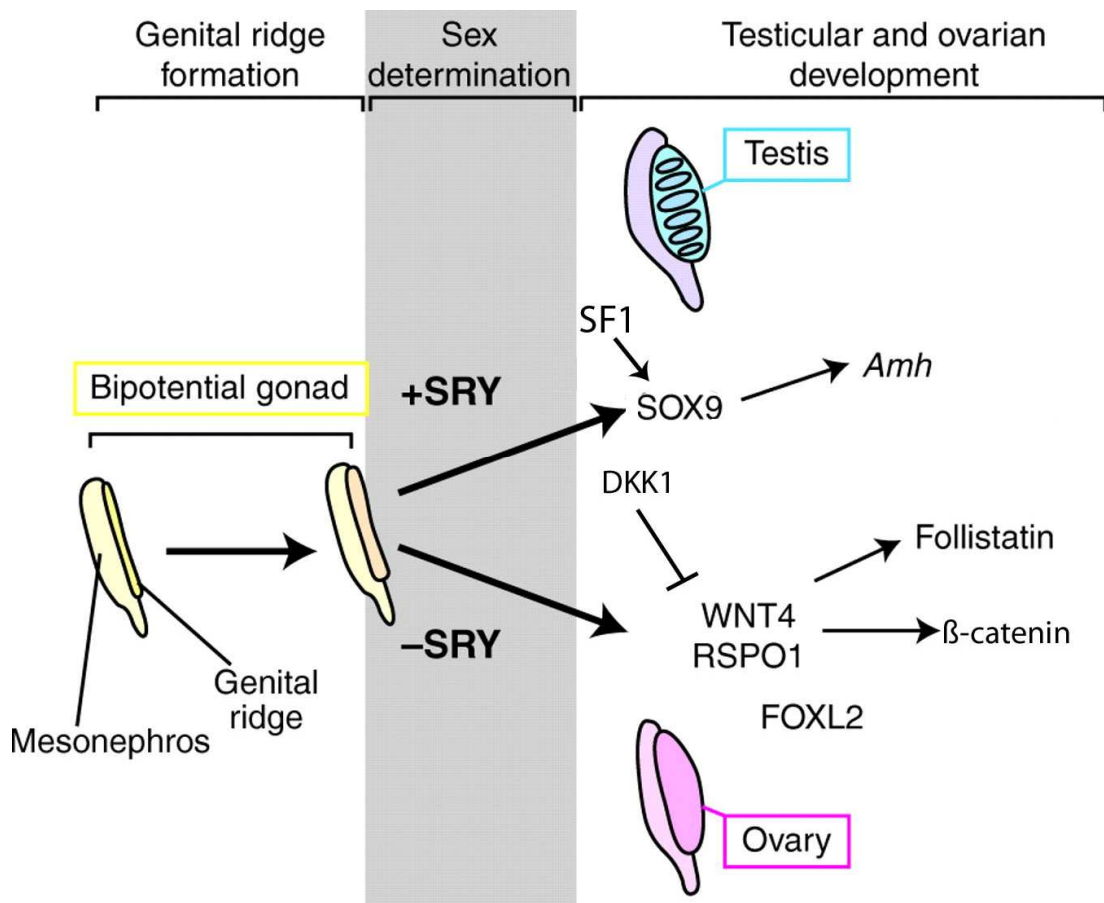


Figure 1.2 Summary of sex determination

Summary of major signalling factors involved in sex determination as discussed in the text. Figure adapted from (Kashimada & Koopman, 2010).

1.3 Fetal Ovarian Development

As the majority of this thesis focuses on ovarian development, further discussion of the literature will be limited to ovarian development and maturation, whereas discussion of testis development will be reserved for later chapters.

1.3.1 Germ Cell Proliferation

Although there is some argument regarding when the population of germ cells in the gonad become oogonia as opposed to PGCs, for this sake of clarity once sex determination has occurred (prior to meiosis) the germ cells in the ovary will be referred to as oogonia in this literature review. The difference is both morphological and based on activity; PGCs are irregular in shape, making them less distinct from interstitial and stromal cells (Gondos *et al*, 1986) and are smaller in size than oogonia (Gosden, 1995; Gougeon, 1996). Mitotically active PGCs express OCT4, rather than the more mature germ cell marker VASA which is expressed from ~12 weeks gestation in the human (Stoop *et al*, 2005; Anderson *et al*, 2007). Oogonia are rounded and can also be identified by globular mitochondria associated with mitotic division (Gondos *et al*, 1986). These oogonia undergo mass proliferation, and by late first trimester, the number of germ cells has increased by ten-fold from the original cohort of PGCs that migrated to the gonad (11 weeks gestation ~240,000; (Bendsen *et al*, 2006)). The oogonia undergo incomplete cytokinesis upon mitotic division (Gondos & Zamboni, 1969), creating clusters of oogonia termed ‘germ cell nests’ or syncytia (de Cuevas *et al*, 1997; Skinner, 2005) connected by cytoplasmic bridges between cells (de Cuevas *et al*, 1997; McNatty *et al*, 2000) which can be seen as early as 10 weeks gestation (Gondos *et al*, 1986) (Figure 1.3). These cytoplasmic bridges allow for the exchange of nutrients between cells and may also be involved in synchronous division (Pepling & Spradling, 1998; Epifano & Dean, 2002). Outwith the germ cell nests, the gonad also contains somatic cell populations which remain fairly unorganised until roughly 12 weeks gestation (Byskov, 1986).

The two main populations of somatic cells in the fetal ovary include the pre-granulosa cells and the mesenchymal stromal cells (in addition to the epithelial lining of the ovary and endothelial cells lining blood vessels). During first trimester, somatic cells and germ cells are arranged in an apparently chaotic manner. However, during proliferation of oogonial nests, the pre-granulosa cells integrate with germ cells becoming part of the oogonial nests and the mesenchymal stromal cells form separate channels or streams amongst the nests (Figure 1.3) (Gondos & Zamboni, 1969; Wartenberg, 1982).

1.3.2 Entry into Meiosis

In late first trimester ~11 weeks gestation, some oogonia progress from mitotic division to meiotic division (Baker & Franchi, 1967; Motta *et al*, 1997), a process which is asynchronous in the human, and occurs progressively through second and third trimester, with oogonia in the interior of the ovary initiating meiosis while oogonia near the epithelium continue to proliferate via mitosis (Skrzypczak *et al*, 1981; Anderson *et al*, 2007). However, in mice this process is more synchronised, with initiation in an anterior-posterior wave occurring between e13.5-15.5 (Menke *et al*, 2003).

One of the first factors implicated in regulation of meiosis was *Dazl*, expression of which is required for germ cells to become meiotically competent (Lin *et al*, 2008). Human studies have identified *DAZZL* mutations associated with subfertility in females (Hertig & Adams, 1967; Lynch & Zhang, 2007) and that another closely related gene *BOULE* may also be involved (Kee *et al*, 2009). *Dazl* up-regulates protein levels of factors necessary for meiosis, including Synaptonemal Complex Protein 3 (*Sycp3*) (Reynolds *et al*, 2007), a component of the synaptonemal complex necessary for the first phase of meiosis (Costa & Cooke, 2007), which also functions in the repair of double-strand breaks during meiotic recombination (Pittman *et al*, 1998; Yoshida *et al*, 1998).

Dazl is also thought to be upstream of stimulated by retinoic acid (*Stra8*), as *Dazl*^{-/-} gonocytes have reduced *Stra8* expression (Lin *et al*, 2008). *Stra8* regulates initiation of meiosis I and is required for pre-meiotic DNA replication (Baltus *et al*, 2006).

Stra8 is activated by retinoic acid (RA) secreted from the mesonephros in the mouse (Di Carlo *et al*, 2000; Bowles *et al*, 2006; Koubova *et al*, 2006; Anderson *et al*, 2008), however recent data indicates *STRA8* expression in the human is reliant on ovarian RA regulation rather than extrinsic sources (Le Bouffant *et al*, 2010; Childs *et al*, 2011). After initiation, prophase I of meiosis progresses through leptotene (chromosome condensation); zygotene (chromosomal pairing); pachytene (initiation of recombination) and diplotene (chromosomes begin to separate but remain attached) before arresting (Baillet, 2011). Arrival at diplotene stage of meiosis I is required for oocyte arrest and the formation of primordial follicles (Hilscher, 1991). Proliferation of all ovarian cell types occurs during early second trimester prior to meiosis, after which oocytes cannot undergo further mitotic replication leaving somatic cells to proliferate further (Fulton *et al*, 2005).

1.3.3 Apoptosis and germ cell nest breakdown

Following nest breakdown all oogonia/oocytes enter one of two fate pathways; they either degrade or they continue to mature and associate with stromal cells to form primordial follicles (Vaskivuo *et al*, 2001). Around the time of meiotic entry, oogonia/oocytes also begin to degrade in a process termed atresia (Kaipia & Hsueh, 1997). Although the exact timing of this event is uncertain, it is thought to initiate between 13-14 weeks gestation (Vaskivuo *et al*, 2001; Hussein, 2005). The number of germ cells that go through degradation prior to birth is great (~80%) resulting in a drastic reduction throughout the remainder of gestation (Baker, 1963; De Pol *et al*, 1997). It is proposed the major mechanism of germ cell degradation is programmed cell death, apoptosis (De Pol *et al*, 1997; Costa & Cooke, 2007). The peak of apoptosis is reported to occur around the initiation of primordial follicle formation (Baker, 1963; Fulton *et al*, 2005) with one to two thirds of oocytes being lost during nest breakdown prior to this process (Pepling & Spradling, 2001; Bristol-Gould *et al*, 2006). It is hypothesised this clearing of germ cells acts as a quality control measure, eliminating oogonia exhibiting chromosomal or mitochondrial defects (Tilly, 2001). This is supported by high levels of germ cell apoptosis in fetuses with chromosomal abnormalities (Modi *et al*, 2003; Di Giacomo *et al*, 2005; Hunt & Hassold, 2008) or mitochondrial deficiencies (Perez & Sanville, 2000).

During human fetal ovarian development, the majority of the cells detected undergoing apoptosis are indeed germ cells (Vaskivuo *et al*, 2001; Abir *et al*, 2002; Hussein, 2005), with four main factors identified in the regulation of apoptosis; BCL-2 associated X protein (BAX) and BCL-2 associated agonist of cell death (BAD) as pro-apoptotic factors, and B-cell lymphoma/leukemia-2 (BCL-2) and myeloid leukaemia sequence-1 (MCL-1) as anti-apoptotic (Boise *et al*, 1993; Tilly, 1996). BAX and BAD are expressed in somatic and germ cell populations; whereas BCL-2 and MCL-1 were exclusively located in the somatic and germline respectively (Hartley *et al*, 2002). *BCL-2* expression is seen as early as 6 weeks gestation (Quenby *et al*, 1999) and is maintained until roughly 18 weeks gestation (Albamonte *et al*, 2008), at which time, *MCL-1* is highly expressed and may play a role in the inhibition of cell death after follicle assembly (Hartley *et al*, 2002). These factors interact with the pro-apoptotic factors to determine cell fate (Hsu *et al*, 1997). The pro-apoptotic factor *BAX* is expressed from week 12 of gestation onwards, and with expression not restricted like that of *BCL-2* (Vaskivuo *et al*, 2001; Hartley *et al*, 2002; Albamonte *et al*, 2008). Protein expression of BAX as determined via immunohistochemistry was also seen to be more intense and stable than that of BCL-2 after initiation of meiosis, which is consistent with the onset of apoptosis (Albamonte *et al*, 2008).

It is thought the pro-apoptotic members BAX and BAD function via dimerization, increasing mitochondrial permeability and forming large channels within targeted cells, resulting in release of cytochrome c from the mitochondria and activating caspases (Cory & Adams, 2002). This is supported by the detection of cleaved caspase-3 (the active form of this pro-apoptotic caspase) in the human fetal ovary in oocytes before primordial follicle assembly, but is absent in oocytes within primordial follicles (Fulton *et al*, 2005). Observations from mice lacking functional *Bax* also support its role in oocyte apoptosis and nest breakdown, as these animals have three times as many oocytes as their wild-type counterparts (Perez *et al*, 1999). Disruption of *caspase-2* also results in increased primordial follicle number (Bergeron *et al*, 1998).

It is postulated that the purpose of generating of so many ‘unnecessary’ oocytes is to produce additional nutrients and organelles that are then donated to the surviving oocytes via autophagy (Baum *et al*, 2005). This is supported by the finding of mitochondria between oogonia within cytoplasmic bridges (Pepling & Spradling, 2001). The hypothesis behind this mechanism suggests the oocytes remaining after germ cell atresia will have additional cellular resources and are therefore best suited to withstand the decades of meiotic arrest. The autophagy theory is supported by evidence that apoptosis, although likely to be the main cause of germ cell death, cannot account for the large number of germ cells lost during fetal development (Lobascio *et al*, 2007; De Felici *et al*, 2008). Consistent with this theory, various mouse models generated with disruption of autophagy genes display marked reduction in primordial follicle numbers at birth (Gawriluk *et al*, 2011). These data not only support the conclusion that germ cell death is necessary for primordial follicle formation but also that autophagy is a vital pathway for normal fetal ovarian development. Apart from apoptosis and autophagy, clearing of germ cells has also been demonstrated via exfoliation from the ovarian surface epithelium (Motta *et al*, 1997).

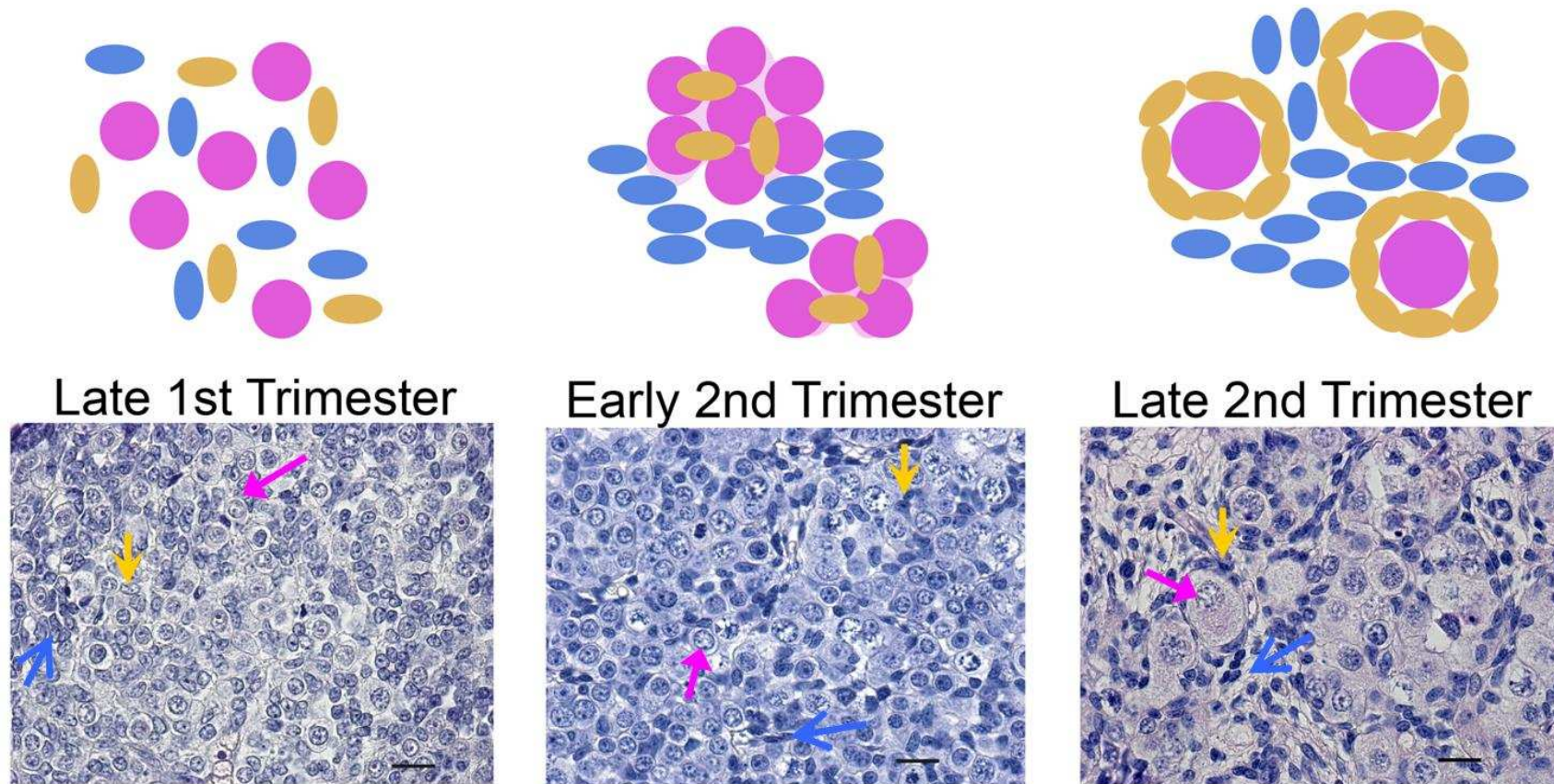


Figure 1.3 Schematic of fetal human ovarian development

(1st trimester) Once germ cells (pink; at this point deemed PGCs) enter the ovary they integrate with mesenchymal stromal cells (blue) and pre-granulosa interstitial cells (orange) in an unorganised fashion. **(Early 2nd trimester)** During a mass mitotic event the germ cells (now deemed oogonia) undergo incomplete division to form germ cell nests with pre-granulosa cells intertwined, after which entering meiosis (now deemed oocytes). **(Late 2nd trimester)** Oocytes grow in diameter as they mature and begin to break away from germ cell nests (as a majority of the oocytes degrade) and associate with pre-granulosa cells to form primordial follicles.

1.3.4 Primordial Follicle Assembly

The breakdown of germ cell nests allows the surviving oocytes (~20%) to closely associate with intermixed pre-granulosa cells (Pepling & Spradling, 2001) (Figure 1.3). During nest breakdown the cytoplasmic bridges are either retracted or degraded via protease action of the pre-granulosa cells (Tingen *et al*, 2009), which form a protective layer around the remaining oocytes. Oocytes that do not associate with pre-granulosa cells to form primordial follicles are lost (Byskov, 1986; McLaren, 1991; Coucouvanis *et al*, 1993; De Pol *et al*, 1997; Pepling & Spradling, 2001). The maturing oocyte with somatic cell association is called a primordial follicle, and although initiation of follicle assembly in the human is reported at different stages in second trimester (Abir *et al*, 2002; Sforza *et al*, 2003), our laboratory reports the onset of primordial follicle formation to occur around 18 weeks gestation (Fulton *et al*, 2005). The primordial follicle complex is then enclosed in an individual basement membrane (Rajah *et al*, 1992) separating it from the mesenchymal stromal cell environment (Figure 1.3).

In the mouse fetal ovary, breakdown of germ cell nests allowing for primordial follicle formation is governed by estrogenic signalling (Iguchi *et al*, 1986). During gestation the fetal oocytes are exposed to maternal estrogen which keeps oocytes within germ cell nests (Kezele & Skinner, 2003; Chen *et al*, 2009), at parturition this signalling is removed signalling for the nests to breakdown which allows for primordial follicle formation via the integration of pre-granulosa cells into germ cell nests allowing for association with oocytes. Exposure to estrogenic signalling postnatally results in multiple oocyte follicles or MOFs (Jefferson *et al*, 2002), which are created by the disruption of nest breakdown; whereas premature removal from estrogenic signalling results in premature nest breakdown (Chen *et al*, 2007b). However, in the human, although estrogen receptors are present (Fowler *et al*, 2011) primordial follicle formation occurs during mid-gestation, and thus removal of maternal estrogen is not possible as a signalling cue for germ cell nest breakdown highlighting another species-specific difference during ovarian development.

However, the non-human primate, like the human, initiates primordial follicle formation during mid-gestation, and thus has served as a good model for identifying possible estrogenic roles in fetal follicle formation. A recent baboon model of estrogen deprivation during *in utero* development, resulted in a significant reduction in primordial follicle number, suggesting estrogen does play a role during fetal ovarian development (Zachos *et al*, 2002). Further studies demonstrated estrogen regulates several factors important for primordial follicle formation, including the ratio of Activin : Inhibin expression, development of oocyte microvilli, and expression of the transferrin receptor (Billiar *et al*, 2003; Billiar *et al*, 2004; Zachos *et al*, 2004; Zachos *et al*, 2008). Further, estrogen is able to directly regulate baboon oocytes via estrogen receptor β (ER β), but estrogen receptor α (ER α) is not expressed (Bocca *et al*, 2008).

Arrested oocytes within primordial follicles remain quiescent until recruitment for growth and ultimately ovulation later in life, and are reliant on stromal support to maintain the follicle throughout the female's reproductive lifespan, which in the human lasts some 3 decades (Pincus & Enzmann, 1935; Borum, 1961; Maheshwari & Fowler, 2008).

1.4 Alternate sources of follicles during adulthood?

It is widely accepted that the number of follicles a female produces during fetal life will determine the number of follicles that she will have for ovulation during adulthood (Morita & Tilly, 1999a). There are however, reports purporting the existence of female germ-line stem cells in the adult ovary (Johnson *et al*, 2004), from which primordial follicles could potentially be derived postnatally. In these reports, it is postulated that ovarian germline stem cells could be located in the surface epithelium of the ovary or in bone marrow (Johnson *et al*, 2004; Johnson *et al*, 2005). Subsequent studies from other groups have demonstrated bone marrow is not involved in the formation of functional oocytes (Eggan *et al*, 2006), but factors from the bone marrow may regulate the growth of new oocytes especially following ovarian damage (Lee *et al*, 2007).

More recently, cells purported to be germline stem cells have been isolated from the ovarian epithelium of adult and prepubertal mice via immune-magnetic isolation of MVH/VASA positive cells (Zou *et al*, 2009). The isolated cells were cultured for ~6 months, allowing for all non-proliferating (meiotic) cells to perish leaving only MVH positive mitotic cells; the cells were then infected with a GFP virus and transplanted into the ovaries of sterilised recipient female mice. Upon further analysis, recipients had GFP positive oocytes within follicles at all stages and bore offspring, 28% of which were GFP positive (Zou *et al*, 2009).

Although, this research is exciting, as it suggests a pool of oogonia which could maintain fertility outwith the finite cohort of primordial follicles formed at birth, it seems unlikely this is the full story, as several animal models (as referenced in (Skinner, 2005) and women (Telfer *et al*, 2005) fail to demonstrate any replenishment of this cohort of follicles. Indeed, initial studies reported isolated ovarian stem cells to be few per ovary (Johnson *et al*, 2004; Tilly *et al*, 2009). Additionally, it is unclear how these studies in rodent models equate to human physiology. Therefore, the relevance of ovarian stem cells remain to be further elucidated. Additionally the existence of functional stromal cells including granulosa stem cells *in vivo* would need to be considered, as follicle formation would require more than just an oocyte in cases of severe ovarian damage (Tilly & Telfer, 2009).

1.5 Repercussions of fetal follicle formation

Consistent with the currently accepted theory that primordial follicles determine the cohort of oocytes ovulated in adulthood, failure to form sufficient primordial follicles during fetal life results in premature ovarian insufficiency (POI) or infertility (Mattison *et al*, 1983; Byskov, 1986; Byskov *et al*, 2005). Although the field is progressing, POI remains relatively common, occurring in 1% of women (Coulam, 1986; Goswami, 2005). Primordial follicle regulation and preservation are also of interest in current cancer therapies, as intensive courses of either radio- or chemotherapy can result in the loss of primordial follicles leading to infertility (Sonmezer & Oktay, 2004). Understanding the process of primordial follicle formation and ovarian development during fetal life could provide insight into what factors influence the cell fate decisions of apoptosis vs. survival, which in turn could be manipulated for clinical use.

1.6 Known Regulation of Fetal Germ Cell Development

Various factors have been identified as important for germ cell development leading to primordial follicle formation. The following section will briefly discuss both secreted factors that effect ovarian cells via classical ligand-receptor signalling deemed growth factors, as well as transcription factors, which regulate ovarian development via modulation of transcription of other genes. These two groups of regulators work in concert to coordinate early ovarian development leading to primordial follicle formation.

1.7 Growth factors

Growth factors are signalling molecules which function via receptor binding to activate intracellular signalling cascades in order to regulate critical cellular functions including; proliferation, differentiation, cell survival and apoptosis (Bianco *et al*, 2006). Several growth factors have been established as regulators of fetal ovarian development and will be described in the following section (Figure 1.4).

1.7.1 Kit ligand (KL)

As previously discussed, KL via its receptor c-kit, regulates PGCs migration and survival during gonad formation as demonstrated in the mouse (Godin *et al*, 1991; Pesce *et al*, 1993a). PGCs express c-kit before they leave the hindgut (Runyan *et al*, 2006; Gu *et al*, 2009), and allows for direct KL regulation after germ cell specification. It is thought KL functions as a chemoattractant during this process, guiding PGCs to the gonads (Farini *et al*, 2007). This role was confirmed in the homozygous null murine models for either *KL* or *c-kit*, which result in disrupted migration and complete loss of the PGC cohort ((Mintz & Russell, 1957; McCoshen & McCallion, 1975) as discussed in (Edson *et al*, 2009)).

Although early data regarding KL's role in regulation of migration is not available in the human fetal ovary, it is known after gonad formation KL is expressed by mesenchymal stromal cells and the pre-granulosa cells closely associated with oogonia (Hoyer *et al*, 2005). It is hypothesised KL acts to prevent precocious entry into meiosis at this point in ovarian development (Coutts *et al*, 2008; Childs & Anderson, 2009), allowing for continued proliferation via mitosis, which is consistent with the down-regulation of c-Kit expression around the initiation of meiosis entry. Expression of c-Kit is resumed around initiation of follicle formation, and thus it is further thought to maintain meiotic arrest until follicle activation (Vainio *et al*, 1999; Jaaskelainen *et al*, 2010). *In vitro* study of rodent oocytes demonstrated that KL is able to up-regulate PI3/AKT, which functions to suppress Foxo transcription factors (such as Foxo3a which will be discussed in a subsequent section) (Reddy *et al*, 2005). Foxo3A is known to regulate follicle activation, and

thus KL's regulation of this factor may orchestrate follicle development as well as maintenance of follicle arrest (Castrillon *et al*, 2003).

Expression of c-Kit is down-regulated upon germ cell nest formation but is up-regulated in oocytes after meiotic division (Robinson *et al*, 2001; Stoop *et al*, 2005). This expression pattern is consistent with the hypothesis that KL signalling is important for regulation of oocytes later in ovarian development. In order to study KL effects, without perturbing initial migration and survival of PGCs, an anti-murine c-kit antibody, ACK2, was injected to female mice at different points during gametogenesis to inhibit c-kit function and to elucidate possible KL functions in later gestation (Yoshida *et al*, 1997). This study determined blockade of KL/c-kit interaction at birth (initiation of primordial follicle formation) did not result in a disruption of primordial follicle formation, rather it affected granulosa cell proliferation, thereby affecting further follicular development. However, conflicting data gathered from *in vitro* culture of fetal murine ovaries demonstrates KL treatment is able to accelerate primordial follicle formation (Wang & Roy, 2004). Thus KL's role in fetal ovarian development post-migration remains unclear.

The human fetal ovary expresses c-Kit in a similar fashion to that established in the mouse, with localisation restricted to mitotic oogonia, diminished in germ cell nests undergoing meiosis, and renewed expression in oocytes within primordial follicles (Robinson *et al*, 2001; Stoop *et al*, 2005). Recent evidence demonstrates KL is inhibited by Activin A in the human fetal ovary, which may prevent precocious primordial follicle formation (Figure 1.5), further suggesting a role for KL in later gestation and demonstrating processes in the fetal ovary are highly regulated by interaction of several growth factors (Childs & Anderson, 2009).

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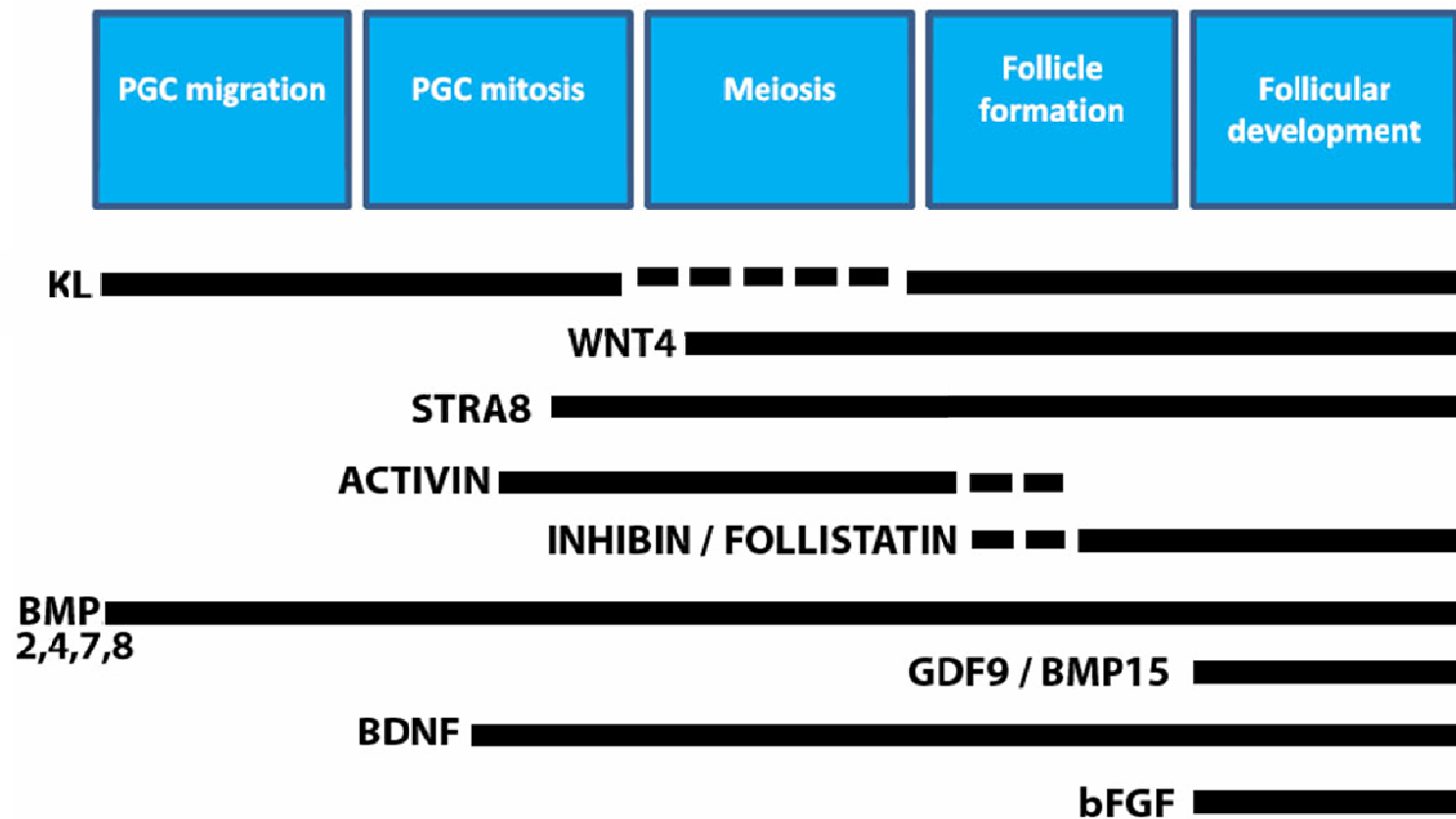


Figure 1.4 *Growth factors important for germ cell maturation and primordial follicle formation*

Several growth factors are identified in regulation of early human ovarian development leading up to primordial follicle formation and beyond, including KL/c-Kit, WNT4, Stra8, Activin, Inhibin, Follistatin, BMP2, 4, 7, 8 and 15, GDF9, BDNF, and bFGF. Expression patterns of each are demonstrated above via a continued line through the gestational period. Repression/down-regulation is depicted as a dashed line. Figure adapted from (Jagarlamudi & Rajkovic, 2011).

1.7.2 Wnt4

Wnt4 action is essential for sex determination, but it has also been demonstrated to regulate other processes in the fetal ovary. Wnt4 expression in the fetal female mouse is restricted to pre-granulosa cells of the developing ovary and is also expressed in the mesonephros (Vainio *et al*, 1999; Jaaskelainen *et al*, 2010). Wnt4's role in reproductive development was investigated in female mice homozygous null for the *Wnt4* allele, which were found to be partially sex reversed with male-like steroidogenic cells (Vainio *et al*, 1999; Heikkila *et al*, 2005). In addition *Wnt4*^{-/-} ovaries also had a distinct coelomic vessel, similar to that seen in the testis (Jeays-Ward *et al*, 2003) with associated Wolffian rather than Müllerian ducts (Vainio *et al*, 1999). Thus Wnt4 represses the male pathway, later demonstrated to be via downstream β -catenin and follistatin signalling (Yao *et al*, 2004).

However, in addition to the clearly defined role in sex determination, *Wnt4*^{-/-} ovaries also had marked reduction in oocyte number after e14.5 (post-migration, proliferation, and meiosis), which was not seen in *Wnt4*^{-/-} males (Heikkila *et al*, 2005), demonstrating *Wnt4* plays a role in oocyte-specific survival and development. Further investigation demonstrated a rapid depletion of ~90% of oocytes around e16 (Yao *et al*, 2004) and that remaining follicle structures displayed disrupted morphology (Vainio *et al*, 1999). Further, *Wnt4* expression is notably heightened in fetal ovaries around initiation of primordial follicle formation, a timepoint which is also associated with a decline in apoptosis (Vaskivuo *et al*, 2001), suggesting a role in the regulation of oocyte survival. However, investigation of this hypothesis demonstrated no change in expression of apoptotic factors in *Wnt4*^{-/-} ovaries, suggesting regulation of oocyte survival via Wnt4 is may be downstream of another mechanism (Jaaskelainen *et al*, 2010).

In the human fetal ovary, WNT4 is expressed by the pre-granulosa cells, but is also expressed by oocytes, with increased expression during initiation of primordial follicle formation (Jaaskelainen *et al*, 2010). Despite this difference in localisation, loss of function mutation of *WNT4* in humans mimics the sex reversal seen in the *Wnt4*^{-/-} mouse model, with excess androgens noted as well as masculinisation of reproductive organs (Biason-Lauber *et al*, 2004); demonstrating *Wnt4*'s role in gonad development is likely conserved between species.

1.7.3 Retinoic Acid

Retinoic acid (RA) is an active derivative of vitamin A, and functions via the nuclear hormone receptors RAR- α , - β , - γ , and RXR- α , - β , - γ (Bowles *et al*, 2006; Koubova *et al*, 2006), which are localised primarily to the germ cells of both male and female gonads in the mouse and human (Morita & Tilly, 1999b; Le Bouffant *et al*, 2010; Childs *et al*, 2011). RA is able to promote the onset of meiosis during fetal ovarian development (Bowles *et al*, 2006; Koubova *et al*, 2006), and functions by up-regulating *STRA8*, which is required for DNA replication prior to initiation of meiosis (Baltus *et al*, 2006; Anderson *et al*, 2008). *STRA8* expression increases in both the human and mouse ovary with the onset of meiosis (Menke *et al*, 2003; Houmard *et al*, 2009; Le Bouffant *et al*, 2010).

Although RA is produced by both sexes, data from mice fetal testes homozygous null for a retinoid degrading enzyme *Cyp26b1*, demonstrated this factor is up-regulated in the testis compared to the ovary and is able to metabolise RA (Bowles *et al*, 2006). Based upon this data it was hypothesised that *Cyp26b1* functions to shield male germ cells from RA, thus preventing *Stra8* expression in the testes and the initiation of meiosis. *In vitro* culture of e11.5 murine fetal testes treated with RA seemed to support this, with induced *Stra8* expression and initiation of meiosis (Trautmann *et al*, 2008). However, a recent murine model homozygous null for the RA synthesis enzyme *Raldh2*, which renders the animal unable to synthesise or signal via RA demonstrates these suggested roles may be poorly understood (Kumar *et al*, 2011). *Raldh2*^{-/-} ovaries express *Stra8* and undergo meiosis, and inhibition of *Cyp26b1* in *Raldh2*^{-/-} testes initiates meiosis, all of which occur independently of RA interaction (Kumar *et al*, 2011). These data suggest that although *Stra8* is important for

regulation of meiosis, RA may be unnecessary for its production. In addition the degrading enzyme Cyp26b1 is needed for prevention of meiosis in the testis, but is likely to degrade an RA-like substance rather than RA itself.

Investigation in the human fetal gonad determined RA alone is not able to promote meiosis in fetal testes, again suggesting RA either functions in concert with other factors to initiate meiosis or that it is not involved in this process (Childs *et al*, 2011). However, it is likely meiosis is differentially regulated in the human compared to the mouse, as initiation of meiosis is asynchronous in the human and may require more specific regulation (Childs *et al*, 2011). This hypothesis is supported by the heightened expression of *CYP26B1* in the human fetal ovary compared to the fetal testis (Le Bouffant *et al*, 2010; Childs *et al*, 2011), suggesting this factor may play a different role in the human or may be involved in inhibiting meiosis entry in some cells during ovarian development.

While the roles of RA, Stra8, and Cyp26b1 in meiosis remain to be fully understood, data suggest RA may regulate other functions in the fetal gonad, namely proliferation (Morita & Tilly, 1999b).

1.7.4 TGF- β signalling

The members of the TGF β superfamily have been verified as ovarian regulators in various species. More specifically, the actions of Activin, Inhibin, and the BMPs are essential for fetal ovarian development (Aaltonen *et al*, 1999; Galloway *et al*, 2002; Nilsson & Skinner, 2003; Ross *et al*, 2007b). These cytokines function via serine/threonine kinase receptors to induce intracellular signalling via the SMAD family of proteins (Attisano & Wrana, 1996; Kawabata *et al*, 1999) (Figure 1.5).

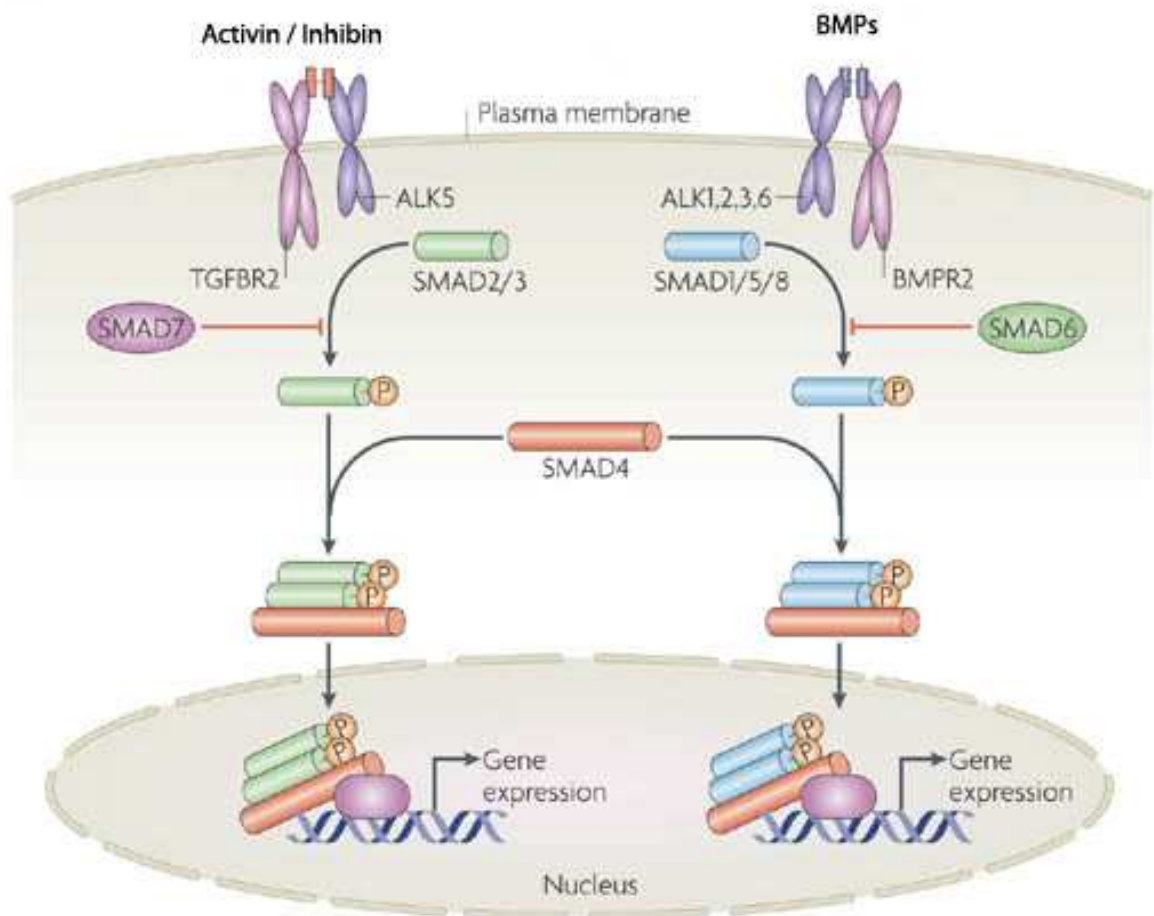


Figure 1.5 Schematic of TGF- β signalling

TGF- β superfamily members signal via Ser/Thr kinase receptors, with Activin and Inhibin utilising TGF β R2 and ALK5 and the BMPs utilising BMPR2 and ALK-1, -2, 3-, and -6. Activated receptors then induce phosphorylation of receptor regulated SMADs, with Activin/Inhibin inducing SMADs 2/3 and BMPs inducing SMADs 1/5/8. Activated receptor SMADs then form heteromeric complexes with the co-transporter SMAD (4) and translocate to the nucleus to regulate gene expression. Phosphorylation of receptor SMADs can be inhibited by inhibitory SMADs (6 and 7), allowing for cell specific regulation of TGF- β signalling. Figure from (ten Dijke & Arther, 2007).

Activin and Inhibin

The Activin/Inhibin family of growth factors are made up of homo- or hetero-dimeric complexes of α and β subunits (Norton *et al*, 1998; Muttukrishna *et al*, 2004), with two isoforms of the β subunit; β A and β B (Trombly *et al*, 2009b). Inhibin is formed by the disulphide-linkage of an α subunit and either β subunit, creating Inhibin A or Inhibin B respectively. Alternatively, Activin formation does not require an α subunit, rather is the homo- or hetero-dimerisation of two β subunits, creating Activin A, Activin B, or Activin AB (Trombly *et al*, 2009b). Inhibin is able to antagonise Activin function via competitive binding of the Activin receptors (Lewis *et al*, 2000), and utilisation of β subunits (McMullen *et al*, 2001). The two components bind Activin receptors which in turn modulate gene expression via Smad2/3 activation and the MAPK pathway (Massague, 1998; Mulder, 2000). However, murine models, created to further elucidate Activin/Inhibin function have been largely inconclusive due to embryonic lethality and overlapping functions of the TGF β family; therefore research in human primary tissue has been vital for determination of Activin/Inhibin function during fetal ovarian development (Matzuk *et al*, 1995; Burns & Matzuk, 2002).

The Activin/Inhibin subunits are expressed by the germ and somatic cell compartments of the human fetal ovary (Rabinovici *et al*, 1991; Harkness & Baird, 1997; Martins da Silva *et al*, 2004). However, the β A subunit is localised solely in the germ cells with increasing expression in larger germ cell (diameter is indicative of oocyte maturation) but expression ceases once oocytes form primordial follicles (Martins da Silva *et al*, 2004). The β B subunit is localised in both germ and stromal cells (Martins da Silva *et al*, 2004) and is expressed in relatively low levels compared to the β A subunit (Rabinovici *et al*, 1991). In contrast, transcript and protein for the α subunit was not detected in the human fetal ovary, determining Activin A and B to be the active Inhibin/Activin regulators during human fetal ovarian development (Martins da Silva *et al*, 2004). However, other studies have demonstrated Inhibin expression in granulosa cells later in follicular development coincident with the reduction in Activin expression (Davis *et al*, 1987). Several of the Activin receptors (ActRIIA, ActRIIB, ALK2, and ALK4) have been localised in the human fetal

ovary, with expression determined in both germ and somatic cells (Coutts *et al*, 2008), demonstrating Activin is able to act in both an autocrine and paracrine fashion.

In support of a role for Activin A in fetal ovarian regulation are data demonstrating regulation of germ cell survival and proliferation in human ovarian culture via downstream SMAD 2/3 signalling (Martins da Silva *et al*, 2004). It is possible that Activin A regulates proliferation and survival via the anti-apoptotic factor MCL-1, as the two factors display similar localisation in the human fetal ovary, but this mechanism has yet to be confirmed (Martins da Silva *et al*, 2004). In addition, Activin A is able to regulate brain-derived neurotrophic factor (BDNF) action, in order to promote germ cell survival via downstream paracrine signalling from pre-granulosa cells (Childs *et al*, 2010a).

Further studies utilising injection of Activin A into neonatal mice resulted in a 30% increase in primordial follicle number (Bristol-Gould *et al*, 2006), suggesting a role in initiation of follicle formation as well as proliferation/survival. Although functional studies regarding Activin A's role in follicle formation have yet to be performed in the human fetal ovary, a possible mechanism has been demonstrated, as Activin A is able to inhibit membrane bound KL expression (Coutts *et al*, 2008; Childs & Anderson, 2009). From this data it is hypothesised that Activin A is able to limit cross-talk between somatic and germ cells by inhibiting KL, thus inhibiting precocious nest breakdown and follicle formation (Figure 1.6) (Childs & Anderson, 2009).

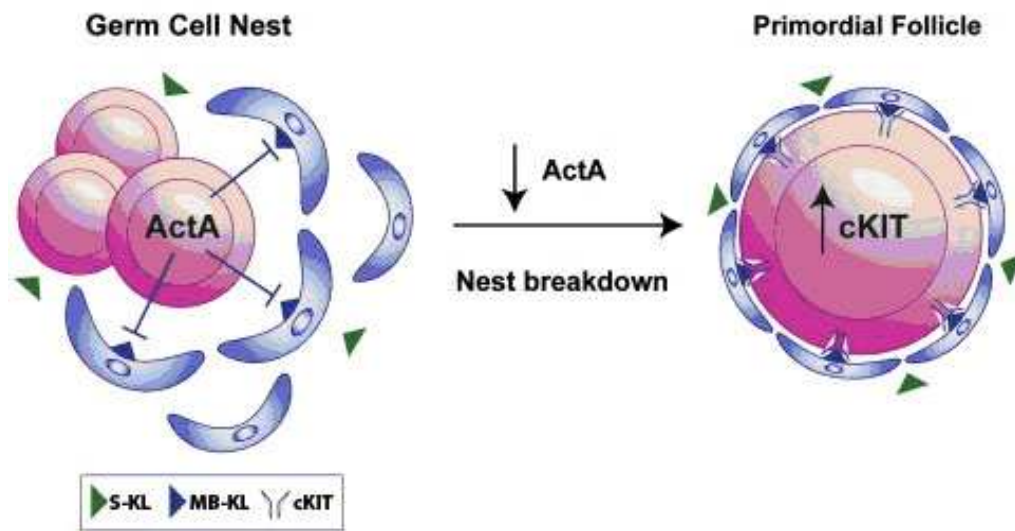


Figure 1.6 Schematic of proposed mechanism of Activin A

Activin A (ActA) is thought to regulate initiation of primordial follicle formation via repression of membrane bound Kit ligand (MB-KL), while allowing signalling via soluble Kit ligand (S-KL). As ActA expression decreases with nest breakdown, this allows for signaling via MB-KL increasing c-KIT downstream signalling and promoting initiation of primordial follicle formation. Figure adapted from (Childs & Anderson, 2009).

Follistatin

Although not a TGF β superfamily member itself, Follistatin mediates some of its ovarian function via interaction with Activin (Hillier & Miro, 1993; Muttukrishna *et al*, 2004). *Follistatin* is expressed by somatic cells in the murine fetal ovary initiating at e11.5 and peaking at e12.5 concomitant with sex determination (Yao *et al*, 2004). Although unrelated to Activin, Follistatin has affinity for and binds Activin repressing its biological effects (Nakamura *et al*, 1990; Schneyer *et al*, 1994). The bound complex is then targeted by cell surface proteoglycans for endocytosis and is degraded (Hashimoto *et al*, 1997). This antagonistic mechanism is noted *in vivo* in several species with Activin expression decreased with increase of Follistatin expression (Schneyer *et al*, 2000; Knight & Glister, 2001), and was confirmed *ex vivo* in the human fetal ovary, with up-regulation of SMAD2/3 signalling with Activin A treatment and down-regulation of this pathway with Follistatin treatment (Coutts *et al*, 2008). Further, three isoforms of Follistatin exist *in vivo* with differing levels of affinity for proteoglycan degradation (Inouye *et al*, 1992; Sugino, 1993). Specific deletion of the *Follistatin* isoform with highest affinity for intracellular degradation in a murine model leads to both reduced litter size and frequency, denoting Follistatin mediated Activin degradation may be important for ovarian biology (Kimura *et al*, 2010).

Follistatin has also been implicated in interaction with another subset of the TGF β superfamily, the BMPs. Although, few data are available regarding this interaction in the fetal ovary, data from various species and tissues suggests Follistatin is able to inhibit the action of BMP2, 4, 7, and 15 (Fainsod *et al*, 1997; Otsuka *et al*, 2001; Glister *et al*, 2004). However, this mechanism remains to be demonstrated in the fetal ovary.

BMPs

The BMPs are also TGF β superfamily factors, of which, BMP2, 4, 7, 8, 15 and growth differentiation factor 9 (GDF9) are of particular interest during fetal ovarian development. Unlike Activin/Inhibin signalling, BMP factors utilise SMADs 1/5/8 for intracellular signalling rather than SMAD 2/3 (Lin *et al*, 2003).

BMP2

Bmp2 expression is restricted to the somatic cells of the fetal ovary post-sex determination in the mouse, which is consistent with the hypothesis it is driven by Wnt4 signalling (Yao *et al*, 2004). *Bmp2* is up-regulated around the time of germ cell nest formation and initiation of meiosis (Kashimada *et al*, 2011), with *in vitro* study of Bmp2 and Foxl2 in an ovarian cell line suggesting these factors may work in cooperation to suppress Follistatin (Kashimada *et al*, 2011).

However, it appears *BMP2* may play a different role in the human fetal ovary. Although function and localisation of BMP2 in the human has yet to be investigated, it is known to signal solely to the germ cells in the human fetal ovary and is developmentally up-regulated prior to primordial follicle formation (Childs *et al*, 2010b) rather than during nest formation and meiosis. It is likely that species-specific differences are involved in the differential regulation seen with several of the Bmp factors.

BMP4

Bmp4 is important for PGC specification and migration. Further studies have identified that inhibition of *Bmp4* in neonatal ovarian culture led to progressive loss of PGCs and that mice homozygous null for *Bmp4* have no germ cells (Lawson *et al*, 1999; Fujiwara *et al*, 2001; Nilsson & Skinner, 2003), it was hypothesised *Bmp4* might also be important for early germ cell survival post-migration (Dudley *et al*, 2007). However, this role was not supported by further work in the mouse (Ross *et al*, 2003) or in the human, where culture of fetal ovary in the presence of BMP4 promoted germ cell apoptosis (Childs *et al*, 2010b). Bmp4 regulation of apoptosis is also evident in development of other organs (Graham *et al*, 1994; Trousse *et al*, 2001). Therefore, it is likely BMP4 regulates germ cell loss in fetal ovarian development rather than survival.

In addition, BMP4 may play a role in inhibition of differentiation, in later ovarian biology, via regulation of the inhibitor of differentiation (*ID*) genes, which are known to regulate apoptosis, proliferation, and differentiation in other tissues (Miyazono & Miyazawa, 2002). Although few published data are available regarding the BMP4/*ID* pathway in the fetal ovary, some reports suggest this pathway may mediate adult ovarian function and that the *Ids* are localised to the granulosa cell complement (Haugen & Johnson, 2010; Hogg *et al*, 2010) .

BMP7

Bmp7 is expressed in the fetal ovary from e10.5 in the mouse, with homozygous mutation resulting in a reduction in PGC number in both sexes (Ross *et al*, 2007b). Additionally *Bmp7* appears to be involved in the primordial to primary follicle transition in the rodent (Lee *et al*, 2001; Lee *et al*, 2004). However, *BMP7*'s role in human fetal development has not been investigated, and levels of *BMP7* transcript are relatively low compared to both *BMP2* and *4*, suggesting it may not be important for ovarian development in the human (Childs *et al*, 2010b).

BMP8

As previously discussed, *Bmp8b* is involved in PGC specification in both sexes, with homozygous deletion resulting in a reduced PGC complement (Zhao *et al*, 1996; Ying *et al*, 2000). However, there are few data clarifying any post-migratory role for *BMP8* during fetal ovarian development.

BMP15 and GDF9

Bmp15 and *Gdf9* are postulated to regulate the ovary in collaboration and display similar structure and expression patterns in the fetal ovary (McNatty *et al*, 2005; Edson *et al*, 2009). However, it is uncertain if their effects are important during fetal development, as expression of both factors is thought to be restricted to oocytes in primary and growing oocytes, with function identified in later stage follicles in cumulus expansion (Dong *et al*, 1996; Aaltonen *et al*, 1999; Nilsson & Skinner, 2002; McNatty *et al*, 2005).

However, both GDF9 and BMP15 expression is detected as early as 16 weeks gestation in the human fetal ovary (Sun *et al*, 2010), suggesting there may be a role for these factors earlier in development. In addition, there have been several reports of mutations in either *GDF9* or *BMP15* in women with POI (Dixit *et al*, 2005; Dixit *et al*, 2006). There is also evidence that Gdf9 may interact with other growth factors involved in fetal ovarian development, including Kitl (Joyce *et al*, 2000; Wang & Roy, 2004). Therefore further evaluation of BMP15 and GDF9 during fetal ovarian development is needed.

Noggin

Noggin, like Follistatin, is not a member of the TGF β superfamily, rather it functions via repression of Bmp signalling (Zimmerman *et al*, 1996; Groppe *et al*, 2002).

Although Noggin is not well characterised *in vivo* in either the fetal mouse or human ovary; recent *in vitro* studies utilising granulosa cell culture have demonstrated Noggin is able to suppress Bmp2 and 4 signalling (Pierre *et al*, 2005; Haugen & Johnson, 2010). Consistent with this hypothesis, mutations in *NOG* (gene encoding Noggin) have been reported in women with POI, suggesting Noggin may affect the primordial follicle pool (Kosaki *et al*, 2004).

1.7.5 Neurotrophins: BDNF and NT4

The neurotrophins are a family of growth factors known to regulate human ovarian development, doing so via their tropomyosin-related kinase (Trk) receptors and the common p75 receptor (Bibel & Barde, 2000). The neurotrophins were initially characterised in the nervous system, where they mediate survival, proliferation and differentiation (Davies, 2000; Bernd, 2008). Consistent with this role, several of the neurotrophin signalling components are expressed in the human ovary, and are developmentally regulated during fetal development (Anderson *et al*, 2002b; Childs *et al*, 2010a).

One of the neurotrophin receptors, TrkB, has increased transcript expression concomitant with primordial follicle formation in mouse (Spears *et al*, 2003), and is localised exclusively to the germ cells of the fetal ovary in both the mouse and the human (Dissen *et al*, 1995; Anderson *et al*, 2002b; Spears *et al*, 2003; Paredes *et al*, 2004). Targeted homozygous disruption of *Ntrk2*, which encodes the TrkB receptor results in reduced germ cell survival and primordial follicle number (Spears *et al*, 2003; Kerr *et al*, 2009), as well as arrest of follicles later in development during the primary to secondary transition (Paredes *et al*, 2004). These results led researchers to investigate further the two main ligands which utilise TrkB for signal transduction, in order to elucidate the ligand that might be regulating these ovarian functions; brain derived neurotrophic factor (BDNF) and nerotrophin-4 (NT4).

In the rodent ovary, both *Bdnf* and *Ntf5* (which encodes Nt4), are expressed across early gestation, with increased *Ntf5* expression compared to *Bdnf*, as well as an increase in *Ntf5* expression around the time of primordial follicle formation (Dissen *et al*, 1995; Childs *et al*, 2010a). Increased expression of *Ntf5* suggests this is the dominant neurotrophin ligand in the mouse fetal ovary; a hypothesis which is supported by unsuccessful attempts to localise *Bdnf* in the fetal mouse ovary, suggesting, as with transcript level, *Bdnf* expression is low (Childs *et al*, 2010a). However, homozygous NT4-deficiency does not result in reduced fertility suggesting it may not be a key regulator of follicle formation (Conover *et al*, 1995).

In the human, *BDNF* and *NFT4* (which encodes NT4) are expressed across gestation in the fetal ovary, with increasing *BDNF* leading to primordial follicle formation (similar to the pattern reported for rodent *Ntf5* expression) (Dissen *et al*, 1995; Childs *et al*, 2010a). BDNF is localised to the somatic cells of human fetal ovary from 9 weeks gestation onwards, and is more strongly expressed by pre-granulosa cells associating with larger oocytes, with a similar expression pattern noted for NT4 (Anderson *et al*, 2002b; Childs *et al*, 2010a). As TrkB receptors are expressed by the germ cells this suggests neurotrophin ligands regulate the oocyte by a paracrine mechanism.

As discussed earlier, Activin A is able to regulate *BDNF* expression in the human fetal ovary, but does not change the expression of *NFT4*; conversely, in the mouse fetal ovary Activin A up-regulates *Nt5* and does not affect *Bdnf* (Childs *et al*, 2010a). Based upon these results and differing transcript expression patterns, it is hypothesised the two neurotrophin ligands BDNF and NT4 may have reversed roles in the rodent and human (Childs *et al*, 2010a). Despite this difference, it appears the role for neurotrophin signalling in regulation of germ cell survival in the mouse (Spears *et al*, 2003; Kerr *et al*, 2009) may also be relevant in the human, as a recent study in the human fetal ovary suggests NT4 increases the number of primordial follicles (Farhi *et al*, 2011). However, this study did not assess the number of naked oocytes in addition to assembled primordial follicles, and therefore it is not possible to elucidate the exact effect of NT4, as increased primordial follicle number could be the result of several mechanisms (such as precocious activation, proliferation and/or survival of oocytes). Therefore, further investigation is necessary to truly understand the roles of the neurotrophins in the human fetal ovary; although the mechanism is likely to be similar to that seen in the mouse, as Activin A, which up-regulates *BDNF* also increases proliferation and survival in the human fetal ovary (Martins da Silva *et al*, 2004).

As functional roles of NT4 and BDNF have yet to explain the phenotype of *TrkB*^{-/-} mice, two other neurotrophins have been examined for their possible reproductive roles: neurotrophin-3 (NT3) and nerve growth factor (NGF), which are expressed along with their receptors in the human fetal ovary (Anderson *et al*, 2002b).

However, data from the mouse determined these factors are not likely to be the ligands signalling via TrkB to regulate fetal ovarian development, as Nt3 regulates primordial to primary transition (Nilsson *et al*, 2009) and that Ngf plays a role in theca cell differentiation (Dissen *et al*, 1995; Dissen *et al*, 2001), with no effects noted in primordial follicles. However, as data from BDNF and NT4 suggests there may be differential regulation of the neurotrophins in the human compared to the rodent, it would be interesting to see if these factors play roles in human fetal ovarian development.

1.7.6 Basic fibroblast growth factor (bFGF)

Basic FGF is of the fibroblast growth factor (FGF) family of growth factors, and is well characterised as a mitogenic factor in the mature ovary, where it is localised to the epithelial and granulosa cells (Gospodarowicz *et al*, 1989; Koos & Olson, 1989; Nilsson *et al*, 2001; Ben-Haroush *et al*, 2005). The function of bFGF during fetal ovarian development has been hypothesised based upon *in vitro* culture of rodent fetal ovaries, which indicate bFGF is able to promote primordial to primary follicle transition (Nilsson *et al*, 2001). Further *in vitro* data suggests bFGF is able to do this via up-regulation of KL (Nilsson & Skinner, 2004).

The function of bFGF remains to be elucidated in the human fetal ovary. However, localisation of bFGF in the human fetal ovary is restricted to oocytes (Koike & Noumura, 1994; Ben-Haroush *et al*, 2005) and transcript expression has been reported across early gestation along with bFGF receptors (Yeh & Osathanondh, 1993; Ben-Haroush *et al*, 2005). The expression of bFGF in primordial follicles is down-regulated upon activation and transition to the primary stage (Quennell *et al*, 2004), suggesting function before this stage. However, it was determined as bFGF expression declines in oocytes, it is up-regulated in the surrounding granulosa and theca cells of primary follicles (Yamamoto *et al*, 1997), suggesting a bi-phasic role for bFGF as the follicle matures.

Although there are more growth factors involved in early ovarian development and germ cell differentiation, the factors described here are the most well described in terms of function and human expression (summarised in Table 1.2).

Table 1.2 Summary of Growth Factor Regulation

Summary of fetal ovarian phenotype from murine models (or function where noted) of key growth factors

Growth Factor	Localisation	Phenotype	Model	Reference
Kit-ligand	GC	Loss of GCs and infertility	Steel mutant mice (homozygous mutation at S1 locus)	(McCoshen & McCallion, 1975)
WNT4	SM	Disruption of sex determination and loss of oocytes	Homozygous null mice	(Heikkila <i>et al</i> , 2005)
Retinoic Acid	SM	No phenotype (although Stra8 and Cyp26b1 both important for regulation of meiosis)	Homozygous null mice	(Kumar <i>et al</i> , 2011)
Activin	GC	Function -GC proliferation, survival and initiation of primordial follicle formation	Human fetal ovarian culture	(Coutts <i>et al</i> , 2008; Childs & Anderson, 2009)
Follistatin	SM	Loss of GCs and subfertility	FST288-only homozygous null mice	(Kimura <i>et al</i> , 2010)
BMP2	GC	Embryonic lethality – reduced PGCs	Homozygous null mice	(Ying & Zhao, 2001)
BMP4	GC	Embryonic lethality – no PGCs	Homozygous null mice	(Lawson <i>et al</i> , 1999)
BMP7	GC	Function in GC proliferation	Homozygous null mice	(Ross <i>et al</i> , 2007a)
BMP8	GC	Embryonic lethality – reduced PGCs	Bmp8b homozygous null mice	(Ying <i>et al</i> , 2000)
BMP15	GC	Subfertility due to ovulation defect	Homozygous null mice	(Yan <i>et al</i> , 2001)
GDF9	GC	Infertile- defect in cumulus expansion	Homozygous null mice	(Yan <i>et al</i> , 2001)
(Neurotrophins) TrkB	GC-TrkB SM- BDNF/NT4	GC loss at primordial stage	TrkB Homozygous null mice	(Spears <i>et al</i> , 2003)
bFGF	SM	Function- activation of follicles past primordial stage	Mouse and bovine ovarian culture	(Nilsson <i>et al</i> , 2001)

1.8 Transcription Factors

Transcription factors work in concert with growth factors to regulate developmental processes in the fetal ovary. Growth factors regulate cell function via ligand-receptor signalling followed by an intracellular cascade, which often modulates transcription factor/s in order to exert function. In turn, transcription factors affect cell function via direct up- or down-regulation of target genes. Transcription factors known to regulate fetal ovarian development are described in detail below (Figure 1.7).

1.8.1 OCT4

OCT4 is a transcription factor from the POU domain family, and is expressed by germ cells in both human and mouse, as early as PGC specification and migration (Rosner *et al*, 1990; Scholer *et al*, 1990; Pesce *et al*, 1998a). OCT4 expression is also found later in gestation, in oocytes undergoing primordial follicle formation; however, its expression is repressed in between these events, with down-regulation occurring around meiosis (Pesce *et al*, 1998a; Pesce *et al*, 1998b; Rajpert-De Meyts *et al*, 2004). It is postulated OCT4 repression may be the result of antagonism by meiotic-specific factors including retinoic acid or its downstream targets (Schoorlemmer *et al*, 1994; Dann *et al*, 2008). It is further hypothesised that Oct4 acts in fetal germ cells as a transcriptional repressor, and may be down-regulated at this time to allow for heightened transcription in the oocytes during the initiation of meiosis (Pesce *et al*, 1998b).

OCT4 is well characterised for its role in maintaining pluripotency in embryonic stem cells (ES cells) (Nichols *et al*, 1998) (Pesce & Scholer, 2000). As ESCs have many phenotypic similarities to the PGC population, it is understandable that OCT4 regulation is also important in germ cells *in vivo* (Pesce *et al*, 1998a; Pesce & Scholer, 2000); however, there are distinct differences between these two cell types and the role of OCT4 in each. In ES cells, OCT4 is characterised for its role in maintenance of pluripotency (Pan *et al*, 2002). However, the PGC-specific deletion of Oct4, utilising CRE/loxP targeting of tissue non-specific alkaline phosphatase ((TNAP) PGC specific marker before e10.5 (Lomeli *et al*, 2000)) in a murine model,

leads to PGC apoptosis (Kehler *et al*, 2004), demonstrating Oct4 regulates survival in PGCs rather than differentiation. The exact functions of OCT4 later in gestation and in the human fetal ovary remain unknown. It has, however been demonstrated that disruption of *OCT4* is associated with gonadal tumours, highlighting actions in the maintenance of gonadal function in the human (Looijenga *et al*, 2003; Rajpert-De Meyts *et al*, 2004).

1.8.2 NANOG

NANOG, like OCT4, is a pluripotency-associated factor in ES cells, and is expressed by PGCs in both human and mouse (Matsui *et al*, 1991; Chambers *et al*, 2003; Mitsui *et al*, 2003; Hart *et al*, 2004; Yamaguchi *et al*, 2005). However unlike OCT4, NANOG is not expressed past the initiation of meiosis (Wang *et al*, 2003a; Yamaguchi *et al*, 2005; Kerr *et al*, 2008). PGC specific deletion of *Nanog*, (utilising TNAP CRE/loxP cross as described for *Oct4*, in addition to a second line utilising an estrogen receptor-CRE) resulted in loss of PGC founder cells, with the remaining PGCs dying during migration (Yamaguchi *et al*, 2009). These results demonstrate *Nanog* is necessary for regulation of PGC survival prior to and during migration, and similarly to Oct4, Nanog does not regulate differentiation as demonstrated in ES cells.

It is postulated Nanog's function in survival of germ cells may be due in part to its regulation of TIA1 cytotoxic granule-associated RNA binding protein-like 1(*Tiall*), a regulator of apoptosis (Taupin *et al*, 1995; Beck *et al*, 1998), oogonia are absent in mice lacking *Tiall* (Beck *et al*, 1998). Nanog may also function via regulation of the Ids (as discuss previously for Bmp4), as Nanog deficient mice demonstrate a down-regulation of *Id1* (Yamaguchi *et al*, 2009), which is known to regulate transcription in ES cells (Kim *et al*, 2008). Finally, although the germ cell-specific *Nanog*^{-/-} murine model (Yamaguchi *et al*, 2009) demonstrated no disruption of migration, recent studies in zebrafish suggest Nanog may regulate PGC expression of Cxcr4, which aids in guiding PGCs to the genital ridge (Sanchez-Sanchez *et al*, 2010), suggesting a role in migration as well as survival. However, it remains to be seen if Nanog regulates CXCR4 in the mouse or human.

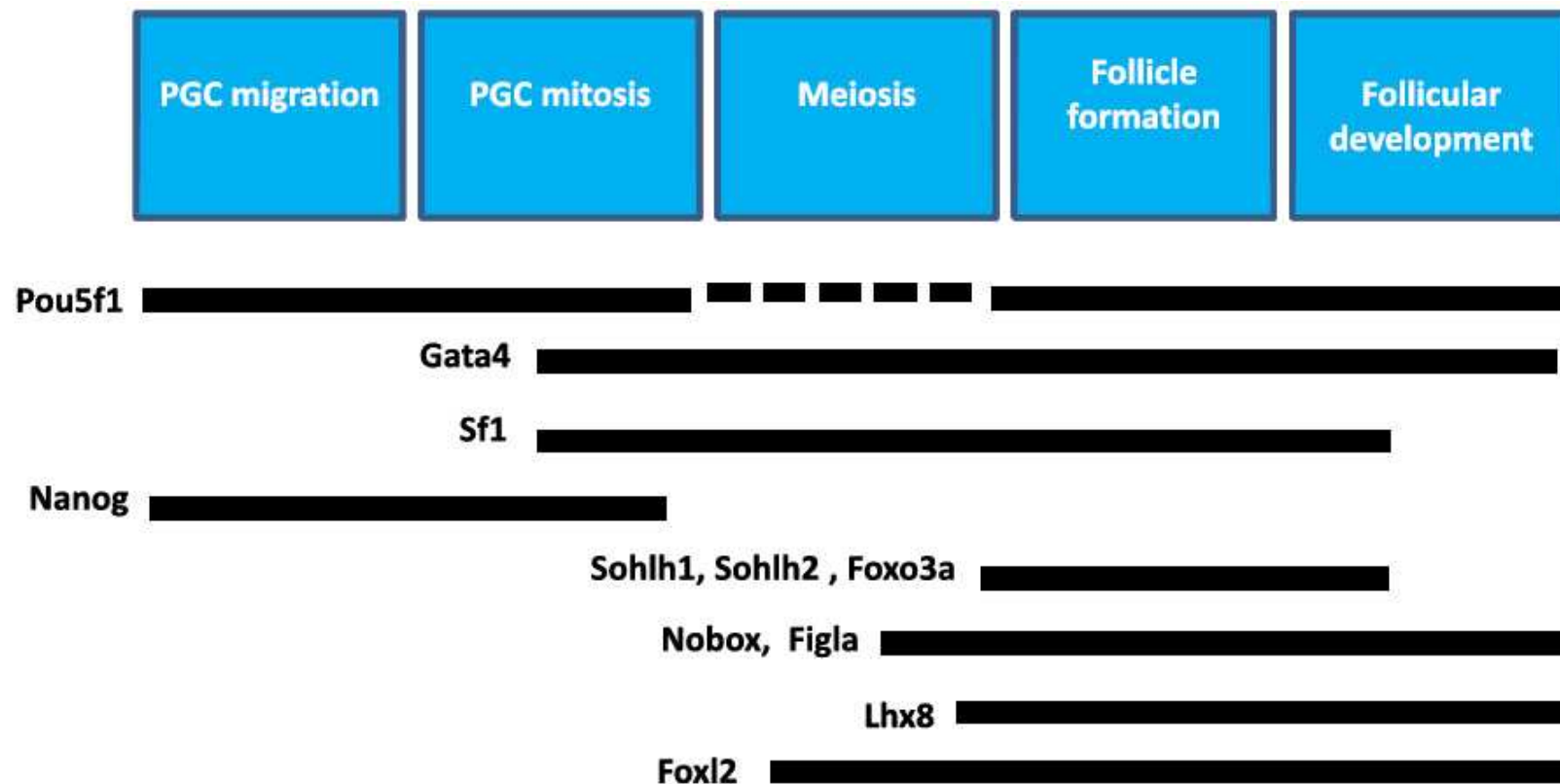


Figure 1.7 Transcription factors important for ovarian development

Several transcriptional regulators are known to be involved in early human ovarian development leading up to primordial follicle formation and beyond, including Pou5f1 (OCT4), GATA4, SF1, NANOG, SOHLH1-2, FOXO3A, NOBOX, FIGLA, LHX8 and FOXL2. Expression patterns of each are demonstrated above via a continued line through the gestational period. OCT4 is repressed during meiosis and thus is depicted as a dashed line during this period. Figure adapted from (Jagarlamudi & Rajkovic, 2011).

1.8.3 Newborn ovary homeobox (NOBOX)

NOBOX is an oocyte-specific homeodomain transcription factor, which is expressed by both the mouse and human in germ cell nests and in oocytes within primordial follicles (Suzumori *et al*, 2002; Huntriss *et al*, 2006). In the mouse, homozygous deletion of *Nobox*, results in germ cell nests which fail to breakdown properly, and rather than forming primordial follicles at birth, entire syncytia undergo atresia (Rajkovic *et al*, 2004; Lechowska *et al*, 2011). *Nobox*^{-/-} ovaries appear to have an occasional primordial follicle, but these oocytes never grow beyond 20 µm and do not recruit the required granulosa cell complement necessary for later activation (Rajkovic *et al*, 2004; Lechowska *et al*, 2011). Complete repression of *Gdf9*, *Bmp15*, and *Oct4* are noted in *Nobox*^{-/-} homozygous null mutants, demonstrating Nobox regulates expression of these genes and possibly others in order to orchestrate its function in ovarian development (Rajkovic *et al*, 2004; Choi & Rajkovic, 2005; Choi *et al*, 2010a). Although direct functional analysis has not been performed in the human, NOBOX is up-regulated during primordial follicle formation (Fowler *et al*, 2009), and mutations in *NOBOX* has also been identified in patients with POI (Qin *et al*, 2007).

1.8.4 LIM homeobox 8 (LHX8)

LIM homeobox 8 (Lhx8) is a LIM homeodomain protein expressed by oocytes in germ cell nests and primordial follicles in the fetal mouse ovary from e13.5 onwards (Pangas *et al*, 2006). Similar to *Nobox*^{-/-} ovaries, homozygous deletion of *Lhx8* results in infertility, with loss of oocytes around initiation of primordial follicle formation (Pangas *et al*, 2006; Choi *et al*, 2008a). Examination at postnatal day (pnd) 0 and pnd7 demonstrated there was no difference in oocyte number in *Lhx8*^{-/-} ovaries compared to wild-type ovaries at birth; although there were significantly fewer primordial follicles, with the majority of oocytes lost in *Lhx8*^{-/-} ovaries before pnd7 (Choi *et al*, 2008a). Expression of *Gdf9*, *Oct4*, and *Nobox* is abolished in *Lhx8*^{-/-} ovaries (Choi *et al*, 2008a), which leads to the suggestion that *Lhx8* might exert some of its effects via direct regulation of *Nobox* (Pangas *et al*, 2006). However, further transcriptome analysis of *Nobox*^{-/-} and *Lhx8*^{-/-} ovaries determined that although several factors were similarly misexpressed, there were distinct regulatory

targets that were not shared between the factors (Choi *et al*, 2008a). One factor distinctly down-regulated in *Lhx8*^{-/-} ovaries was *Kit* and its ligand *Kitl*, which may explain the more severe phenotype when compared to *Nobox*^{-/-} ovaries. However, it is yet to be seen if *LHX8* is important in human primordial follicle formation and oocyte survival, as the *LHX8* mutations identified thus far in human patients have not been associated with a reproductive phenotype (Qin *et al*, 2008).

1.8.5 GATA4

Gata4 is a zinc finger transcription factor involved in sex determination in the gonads, and is normally expressed in the somatic cells of the fetal ovary (Heikinheimo *et al*, 1997; Viger *et al*, 1998; Tevosian *et al*, 2002). In the mouse *Gata4* is expressed from e11.5 onwards, with homozygous ablation resulting in embryonic lethality (Kuo *et al*, 1997; Tevosian *et al*, 2002). It was determined that Gata4 interacts with another somatic factor, Friend of GATA2 (Fog2), to promote the female pathway during sex determination (Tevosian *et al*, 2002). Homozygous deletion of *Fog2* also ends in embryonic lethality (Molkentin *et al*, 1997), but this can be partially rescued by expression of Fog2 in the myocardium, which allows fetuses to develop to ~e17.5 (Tevosian *et al*, 2000). This murine line, in addition to a model utilising a *Gata4* knock-in allele which prevents interaction between Gata4 and Fog2 (Crisponi *et al*, 2001), were utilised to examine Gata4/Fog2 regulation of fetal ovarian development (Manuylov *et al*, 2008). Both murine lines led to disruption of ovarian development in a similar fashion, with PGC depletion, suggesting interaction with Gata4 is the sole cause for the phenotype seen in Fog2 disrupted ovaries (Tevosian *et al*, 2002; Manuylov *et al*, 2008). In addition, *Follistatin* and *Foxl2* are down-regulated and *Inha* and *Dkk1* are up-regulated in both mutant lines suggesting these are likely targets of Gata4/Fog2 action (Manuylov *et al*, 2008).

In the human GATA4 mRNA and protein are localised to the granulosa cells of the fetal ovary, expression of which decreases with gestation (Vaskivuo *et al*, 2001). This pattern of expression has led to the hypothesis GATA4 is likely to function in the human fetal ovary both in sex determination, as well as a protective factor in the

granulosa cells of follicles. However, further investigation is necessary to determine function of GATA4 in the human.

1.8.6 Steroidogenic factor 1 (SF1)

SF1 (NR5A1) is an orphan nuclear receptor expressed by both granulosa and mesenchymal stromal cells of the human and murine ovary (Ikeda *et al*, 1994; Tajima *et al*, 2003). Sf1 expression is noted as early as e9.5 in the fetal mouse ovary and is essential for fetal gonad development and sex determination (Parker & Schimmer, 1997). It is thought Sf1 may regulate these processes via its known targets including *Amh* (Shen *et al*, 1994), *Cyp11a1* and *3 β hsd* (Parker & Schimmer, 1994; LeersSucheta *et al*, 1997). Sf1's role in gonad development was determined via systemic homozygous deletion, which resulted in a lack of gonads and adrenal glands in both male and female offspring (Ingraham *et al*, 1994; Luo *et al*, 1994; Sadovsky *et al*, 1995).

However, in order to dissect ovarian-specific function, Sf1 was disrupted via CRE/loxP mutagenesis utilising the *Amhr-2*/CRE line (limiting deletion to cells of granulosa origin) (Jeyasuria *et al*, 2004; Pelusi *et al*, 2008). Granulosa-specific disruption of *Sf1* led to a decrease in primordial follicle number and a defect in ovulation, rendering the females infertile. However, follicles of all stages were present demonstrating Sf1 plays a role in ovarian development after primordial follicle formation (Jeyasuria *et al*, 2004; Pelusi *et al*, 2008). It was also noted that several proliferative factors (p27 and cyclin D2), aromatase and *Amh* were down-regulated in Sf1 conditional ovaries suggesting these factors are downstream of Sf1 and may be responsible for the defects in follicle number and/or ovulation.

However further investigation is necessary to fully determine Sf1's role during fetal ovarian development, as the *Amhr-2*/CRE conditional model disrupted only granulosa Sf1, with continued expression in interstitial/theca cells which may mask overall Sf1 ovarian function (Jeyasuria *et al*, 2004; Pelusi *et al*, 2008).

In addition, the role of SF1 in the human fetal ovary is unclear. Although several cases of *SF1* disruption have been reported in regards to disruption of male sex differentiation (Coutant *et al*, 2007; Reuter *et al*, 2007; Koehler *et al*, 2008), only one

case of female disruption of *SF1* has been reported, with no change in ovarian function (Biason-Lauber & Schoenle, 2000). However, it has been hypothesised a similar orphan nuclear receptor, liver receptor homolog-1 (LRH-1/NR5A2), may also be able to regulate SF1 targets, and thus masks SF1's function in ovarian biology (Weck & Mayo, 2006).

1.8.7 SOHLH1 and 2

Spermatogenesis and oogenesis specific basic helix-loop-helix 1 and 2 (*Sohlh1* and 2) are basic helix-loop-helix (bHLH) transcription factors, which are expressed in germ cell syncytia and oocytes within primordial follicles in the female, as well as in spermatogonia in the male (Ballow *et al*, 2006; Pangas *et al*, 2006). *Sohlh1* was initially identified along with *Nobox* in an array identifying genes expressed preferentially in oocytes (Rajkovic *et al*, 2001), with *Sohlh2* subsequently identified as a bHLH factor sharing high homology with *Sohlh1* (Ballow *et al*, 2006).

The murine model of homozygous ablation of *Sohlh1* has a similar phenotype to *Nobox*^{-/-} ovaries, losing all follicles by 3 weeks postnatal age (Choi *et al*, 2008b; Toyoda *et al*, 2009). This phenotype is the result of a defect in primordial follicle development rather than formation, as follicles do not progress to the primary stage as a result of disrupted proliferation of pre-granulosa cells (Pangas *et al*, 2006). As a result follicles are lost, which is accompanied by down-regulation of *Gdf9*, *Bmp15*, *Lhx8*, *Kit* and *Nobox* (Pangas *et al*, 2006). Gene expression patterns and phenotype were notably similar to that of *Nobox*^{-/-} ovaries, which led to the hypothesis that *Sohlh1* regulates *Nobox*, as *Nobox* is affected in *Sohlh1*^{-/-} ovaries but no change of *Sohlh1* was determined in *Nobox*^{-/-} ovaries (Pangas *et al*, 2006). Similar comparison of phenotypes was performed in other models leading to the hypothesis that *Sohlh1* also regulates *Lhx8* and *Figla* to varying degrees (Pangas *et al*, 2006; Choi *et al*, 2008a).

Sohlh2 homozygous null ovaries also demonstrate a loss of follicles postnatally; however the phenotype is less severe than seen in either *Sohlh1*^{-/-} or *Nobox*^{-/-} ovaries, with a few follicles progressing to a stage with multi-layered granulosa cells (Choi *et al*, 2008b; Toyoda *et al*, 2009). *Sohlh2*^{-/-} ovaries also demonstrate similar down-

regulation of follicle-associated genes to that seen in *Sohlh1*^{-/-} ovaries, which is not surprising as *Sohlh1* and 2 are able to form heterodimers, and thus may exert their functions in cooperation (Choi *et al*, 2008b; Toyoda *et al*, 2009).

Data regarding SOHLH1 or 2 in the human fetal ovary are limited. Data from azoospermic patients demonstrates the *SOHLH1* human orthologue does play a role in germ cell function (Choi *et al*, 2010b). In addition, up-regulation of *SOHLH1* in mid-gestational fetal ovaries has been determined (Fowler *et al*, 2009). Therefore the role of SOHLH1 and 2 in the human fetal ovary with regards to primordial follicle formation and development, along with possible mutations in POI patients remain of interest.

1.8.8 Factor in the germline alpha (FIGLA)

FIGLA is also a basic helix-loop-helix (bHLH) transcription factor, restricted to the germ cells within the ovary in the mouse and human (Liang *et al*, 1997; Soyal *et al*, 2000; Huntriss *et al*, 2002; Bayne *et al*, 2004). *Figla* was originally characterised as a regulatory factor in the adult ovary via its interaction with the zona pelucida (ZP) proteins (Liang *et al*, 1997; Dean, 2002), which function later in ovarian biology in regulation of plasma membrane formation and fertilisation (Bleil & Wassarman, 1980). However, a murine model of systemic ablation of *Figla* created to investigate this role further demonstrated the resulting homozygous females were unable to form primordial follicles after birth resulting in oocytes loss and infertility (Soyal *et al*, 2000) suggesting an important role for *Figla* in both fetal and adult ovarian biology.

Further investigation determined *Figla* expression peaks at initiation of nest breakdown and follicle formation (Soyal *et al*, 2000; Joshi *et al*, 2007). This increase in expression co-insides with the up-regulation of both *Oct4* and NACHT domain, leucine-rich-repeat domain, and pyrin domain-containing protein 5 (*Nalp5*), which *Figla* is hypothesised to regulate (Soyal *et al*, 2000; Joshi *et al*, 2007). As previously discussed, *Oct4* is highly involved in early PGC development, and is also thought to regulate primordial follicle formation. Function of *Nalp5* in the fetal ovary has yet to be determined, although it expressed specifically by oocytes and is up-regulated with initiation of primordial follicle formation in the mouse (Joshi *et al*, 2007) and human

(Fowler *et al*, 2009). Studies in other tissues suggest Nalp5 may regulate caspase-3 activation and apoptosis, which is consistent with the hypothesis Figla functions to regulate germ cell nest breakdown (Lo *et al*, 2008). In addition to up-regulation of oocytes specific factors, Figla appears to repress testis specific factors and thus may also play a protective role during early ovarian development (Joshi *et al*, 2007; Hu *et al*, 2010).

Up-regulation of *FIGLA* prior to primordial follicle formation was also noted in the human fetal ovary (Huntriss *et al*, 2002; Bayne *et al*, 2004). *FIGLA* is thought to have a similar function in the human fetal ovary, as demonstrated in the mouse, as it is able to regulate the *ZP* genes in a similar fashion (Bayne *et al*, 2004; Fowler *et al*, 2009) to that noted in the mouse, and there are reports of POI patients with mutations in *FIGLA* (Zhao *et al*, 2008).

1.8.9 Forkhead box O3a (FOXO3A)

Foxo3a is a forkhead transcription factor, which is expressed primarily by oocytes within primordial follicles, with further expression in granulosa cells surrounding activated follicles (Liu *et al*, 2007). A murine model homozygous null for *Foxo3* was generated as it was hypothesised the Foxo family of transcription factors were involved in development (Castrillon *et al*, 2003). The resulting animals had several minor physiological abnormalities including anaemia and decreased rate of glucose uptake; however the main phenotypic difference with systemic deletion of *Foxo3a* was a rapid reduction in fertility in female mice, which were completely sterile by 15 weeks of age (Castrillon *et al*, 2003). Further examination of *Foxo3a*^{-/-} females determined no change in ovarian physiology compared to wildtype mice at pnd3, but determined a rapid decline in oocyte number after primordial follicle formation, the result of premature activation of follicles (Castrillon *et al*, 2003).

However, as both germ cell and somatic cells express Foxo3, a tamoxifen-inducible, germ cell-specific *Vasa*-CRE was utilised to further study Foxo3 function specifically in oocytes (John *et al*, 2008). This conditional model developed a similar phenotype to that of the *Foxo3a*^{-/-} ovaries, with global activation of follicles after tamoxifen treatment. It was further demonstrated that *Foxo3a* is activated by

the PTEN-PI3K-AKT signalling pathway (as it is in other systems (Tran *et al*, 2003)), as a similar *Vasa*-CRE conditional deletion of PTEN demonstrated the same phenotype of *Foxo3a* conditional deletion (John *et al*, 2008). An additional murine model was designed to further confirm *Foxo3a* function in oocytes via constitutively activating *Foxo3a* under control of the *Zp3* promoter which is expressed after the primary stage of folliculogenesis (Liu *et al*, 2007). Constitutively active *Foxo3a* results in loss of all follicles at the primary and secondary stage and oocytes display impaired growth (Liu *et al*, 2007). These data determined *Foxo3a* regulates signalling allowing for primordial follicle arrest, and is likely downstream of PTEN-PI3K-AKT signalling as well as Kit (as previously discussed) (Castrillon *et al*, 2003; Hosaka *et al*, 2004; Liu *et al*, 2007; John *et al*, 2008). However, study of the human ortholog of *FOXO3a* in patients with POI has yet to identify a similar function (Watkins *et al*, 2006; Gallardo *et al*, 2008; Vinci *et al*, 2008) and little is known about its expression in the human fetal ovary.

1.8.10 Forkhead box L2 (FOXL2)

Foxl2 is important during sex determination, in the repression of male specific factors (Uhlenhaut *et al*, 2009). FOXL2 is expressed by the pre-granulosa and granulosa cells in the fetal and adult ovary respectively in both the human and mouse (Crisponi *et al*, 2001; Cocquet *et al*, 2003; Duffin *et al*, 2009). Transcript expression of *Foxl2* is increased in mid-gestation in the mouse around the initiation of sex determination, consistent with its established function at this time (Cocquet *et al*, 2003; Duffin *et al*, 2009). Further, functional analysis was performed utilising female mice homozygous null for *Foxl2*, which are infertile as a result of impaired pre-granulosa cell differentiation and basal lamina formation, thereby preventing primordial follicle formation (Schmidt *et al*, 2004; Uda *et al*, 2004). This disruption also leads to a reduction in Activin β a and *Amh* expression (Schmidt *et al*, 2004; Uda *et al*, 2004).

Conditional deletion of *Foxl2* utilising a tamoxifen inducible CRE affecting both granulosa and theca cells (*R26CreERT2*) in the adult mouse ovary resulted in immediate differentiation of these cells to Sertoli and Leydig-like cells, and increased expression of testis markers including *Sox9* and steroidogenic acute regulatory gene (*StAR*) (Pisarska *et al*, 2004; Uhlenhaut *et al*, 2009). This data further demonstrates *Foxl2* acts to repress the male pathway even after initial sex determination and promotes differentiation of granulosa cells necessary for primordial follicle formation.

Interestingly, *FOXL2* is one of the few factors of the germ cell niche originally identified in the human, with mutation identified in humans patients with blepharophimosis ptosis epicanthus inversus syndrome (BPES I and II), which includes ovarian failure or subfertility (Crisponi *et al*, 2001; Prueitt & Zinn, 2001; Cocquet *et al*, 2002b; Cocquet *et al*, 2003). Non-BPES mutations of *FOXL2* have also been reported with ovarian dysfunction (Harris *et al*, 2002). Both *FOXL2* localisation and gene expression patterns in the human fetal ovary are comparable to that seen in the mouse, with initiation of *FOXL2* expression before 8 weeks gestation and up-regulated at 14-15 weeks gestation (Duffin *et al*, 2009). However, *FOXL2* function in the human fetal ovary has yet to be confirmed.

This is a summary of the established transcription factors (Table 1.3) identified as regulators in the fetal ovary and female germ cell development.

Table 1.3 Summary of Transcription Factor Regulation

Summary of fetal ovarian phenotype from murine models (or function where noted) of key transcription factors

Transcription Factor	Localisation	Mouse Phenotype	Mouse Model	Reference
Oct4	GC	PGC loss - infertility	PGC-specific CRE/Lox	(Kehler <i>et al</i> , 2004)
Gata4	SM	PGC loss - infertility	Gata4 ^{ki} – inhibits Gata4/Fog2 interaction	(Manuylov <i>et al</i> , 2008)
Sf1	SM	PGC loss - infertility	FTz-F1 disruption which codes for Sf1 protein	(Luo <i>et al</i> , 1994)
Nanog	GC	PGC loss - infertility	PGC-specific CRE/Lox	(Yamaguchi <i>et al</i> , 2009)
Sohlh1 and Sohlh2	GC	Primordial to primary block –sterile	Homozygous null	(Pangas <i>et al</i> , 2006; Choi <i>et al</i> , 2008b)
Foxo3a	GC	Global activation of follicles –sterile	Homozygous null	(Castrillon <i>et al</i> , 2003)
Nobox	GC	Primordial to primary block –sterile	Homozygous null	(Rajkovic <i>et al</i> , 2004)
Figla	GC	Primordial follicle block - infertility	Homozygous null	(Soyal <i>et al</i> , 2000)
Lhx8	GC	Primordial to primary block –sterile	Homozygous null	(Choi <i>et al</i> , 2008a)
Foxl2	SM	Loss of follicles due to somatic fault –sterile	Homozygous null	(Uda <i>et al</i> , 2004)

1.8.11 Germ cell niche and other factors

Growth factors (illustrated in Tables 1.2 and Table 1.4) extracellular matrix proteins, and hormones, allow for crosstalk between the germ cells and neighbouring cells in the human fetal ovary, which in turn initiates intracellular signalling and modulation of transcription factors (Table 1.3) in order to regulate ovarian biology and germ cell development.

The paracrine, juxtacrine and autocrine support provided via these factors creates the microenvironment necessary for germ cell development and function and is termed the ‘germ cell niche’ (McLaren, 1991; De Felici, 2000). This term refers to the signalling milieu that is necessary to sustain the germ cell progression allowing for normal fertility in adulthood. However, the full cohort of growth and transcription factors involved in ovarian development remain unknown. Primordial follicle formation is important for future fertility, thereby making the determination of the factors within the germ cell niche and their interactions essential.

Table 1.4 Other factors that may be involved in fetal ovarian development

Summary of fetal ovarian phenotype from murine models (or function where noted) of other factors possibly involved in fetal ovarian development

Factor	Hypothesised function	Model	Reference
Notch	Regulates follicle formation	Mouse organ culture	(Trombly <i>et al</i> , 2009a)
Nalp5	Involved in primordial follicle formation	Abscent in <i>Figla</i> ^{-/-} mice Up-regulated in 2 nd trimester human fetal ovary	(Joshi <i>et al</i> , 2007) (Fowler <i>et al</i> , 2009)
Wt1	Regulates gonad formation	Homozygous null mice	(Kreidberg <i>et al</i> , 1993)
Zglp1	Regulates GC survival	ZGLP-1 (<i>lacZ</i>) null mice	(Li <i>et al</i> , 2007)
Lhx9	Regulates PGC survival	Homozygous null mice	(Birk <i>et al</i> , 2000)
Pod1	Regulates of gonad structure	Homozygous null mice	(Cui <i>et al</i> , 2004)
Aromatase	Regulates follicle formation	Homozygous null mice	(Britt <i>et al</i> , 2004)
AMH	Regulates primordial follicle activation	AMH levels in humans relates to follicle number Mouse organ culture	(de Vet <i>et al</i> , 2002; Durlinger <i>et al</i> , 2002)
Aryl-hydrocarbon receptor	Regulates primordial follicle number	Homozygous null mice	(Benedict <i>et al</i> , 2000; Robles <i>et al</i> , 2000)

1.9 Possible regulators of early ovarian development

Several questions remain regarding the established factors of the germ cell niche and whether other unidentified factors are involved during fetal ovarian development. Several factors are known to regulate similar mechanisms in other tissues (proliferation, differentiation, apoptosis, etc), and interact with established ovarian regulators. In addition, these factors are known to be vital to adult ovarian function. However, their roles during fetal ovarian development and interaction with the germ cell niche are unknown. The following sections will describe these regulatory factors postulated to be involved during fetal ovarian function.

1.9.1 Prostaglandin E2

The prostaglandins (PGs) are lipid mediators classically characterised as regulators of inflammation, immunity, and vascular homeostasis (Murakami *et al*, 1993). Their signalling is known to promote angiogenesis, inhibit apoptosis, and increase proliferation and migration (Sales & Jabbour, 2003a), with regulation determined in various species ranging from invertebrates to humans denoting their roles are generally evolutionarily conserved (Cha *et al*, 2006). PGs came into the limelight in the clinical world in the early 1970's, with non-steroidal anti-inflammatory drugs (NSAIDs) which reduce inflammation symptoms including swelling, pain and fever by inhibiting PG synthesis (Vane, 1971).

PGs are synthesised by the conversion of arachadonic acid by cyclooxygenase enzymes (COX1 and COX2). In a physiological sense, COX1 is traditionally thought of to be the ubiquitously expressed "maintenance" enzyme, whereas COX2 is important for cytokine mediated specific events. This is supported by constitutive expression of COX1 in several organs (kidney, lung, stomach, colon) and the inability to stimulate COX1 levels *in vitro* (Kargman *et al*, 1996), whereas COX2 expression is not constitutively expressed in most tissues but can be rapidly induced by cytokine or growth factor expression (Cha *et al*, 2006).

The COX enzymes produce prostaglandin H_2 (PGH_2), which is further converted to prostaglandin D_2 , E_2 , $F_{2\alpha}$, thromboxane (TXA_2 or TXB_2) or prostacyclin (PGI_2) by specific terminal prostanoid synthase enzymes, such as prostaglandin E synthase (PTGES) (As shown in Figure 1.8). In addition, although the mechanism remains unclear, genetically modified murine models have demonstrated the COX enzymes may preferentially synthesize specific prostaglandins (as further described below). It is also notable that the PGs and COX2 are able to signal in both an autocrine and paracrine fashion that results in a positive-self-sustaining feedback loop (Sales & Jabbour, 2003b).

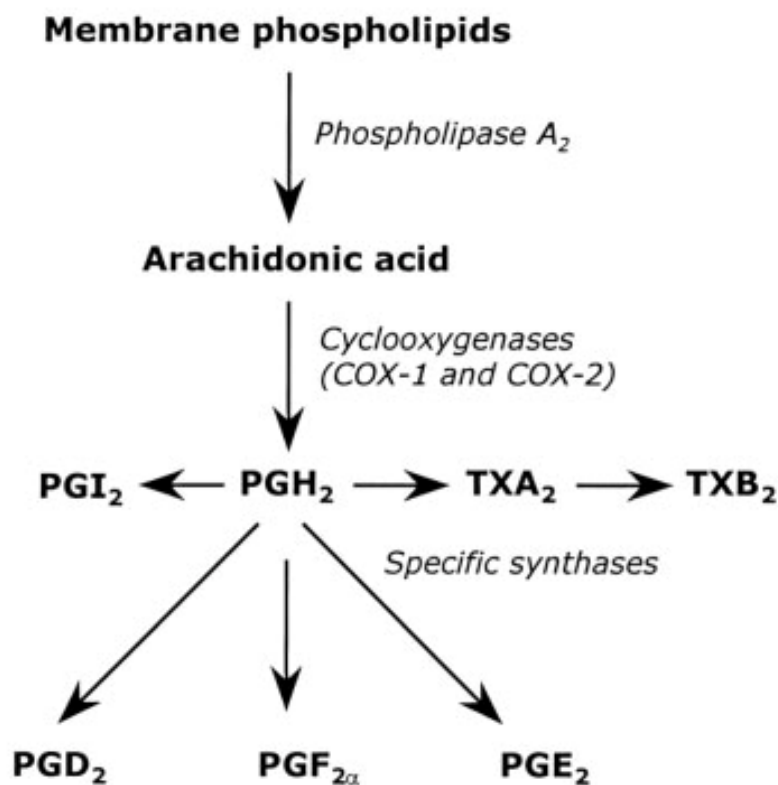


Figure 1.8 Arachidonic acid to prostaglandin pathway

As fully described in the text, PGE_2 is synthesised from a stepwise enzymatic pathway initiating with breakdown of phospholipids and resulting in several prostaglandins (D_2 , $F_{2\alpha}$, and E_2), thromboxane (TXA_2 and TXB_2) and prostacyclin PGI_2).

Even before PGs were identified, several scientific groups had determined there was a lipid mediator in semen (now known to be PGs) that causes contraction of the uterine smooth muscle and reduced blood pressure (Cha *et al*, 2006). For this reason, the PGs were isolated and characterised as regulators of reproductive inflammatory events, including parturition, ovulation, menstruation and endometriosis, as well as fertilisation, implantation and decidualisation (Behrman, 1979; Oates *et al*, 1988a; Oates *et al*, 1988b; Baird *et al*, 1996; Sales & Jabbour, 2003b).

Studies using animal models have further defined these roles, with homozygous ablation of *COX1* in female mice resulting in prolonged gestation and parturition, with normal ovulation and fetal development (Langenbach *et al*, 1995). The reproductive phenotype could also be rescued with administration of $\text{PGF}_{2\alpha}$ (Gross *et al*, 1998), suggesting this may be the dominate PG product of COX1. In contrast, *COX2* homozygous null females result in a more severe reproductive phenotype, including failure to ovulate, fertilise, implant, and decidualise (Dinchuk *et al*, 1995; Lim *et al*, 1997). However, the ovarian phenotype was rescued with the administration of PGE_2 (Lim *et al*, 1997). Despite both precursor enzymes catalysing the same reaction and some level of redundancy confirmed (Wang & Roy, 2004), it is apparent from these models that the COX enzymes may catalyse different amounts of each prostaglandin leading to different downstream outcomes. Unfortunately, overall effects of complete ablation of the COX enzymes cannot be investigated as double-knockout mice die shortly after birth due to patent ductus arteriosus (Loftin *et al*, 2001).

However, specific *COX*^{-/-} models have identified PGE_2 and $\text{PGF}_{2\alpha}$ as the two main PGs responsible for of the above reproductive phenotypes, and therefore the most involved in reproductive function. Further investigation led to the ablation of the $\text{PGF}_{2\alpha}$ receptor, which resulted in a mouse model that loses parturition function, whereas ablation of one of the PGE_2 receptors results in disruption of ovulation (Hizaki *et al*, 1999; Kennedy *et al*, 1999; Tilley *et al*, 1999; Narumiya & FitzGerald, 2001). From this evidence it is apparent that PGE_2 may be the more important PG in ovarian function.

PGE₂ functions in the adult ovary in initiation of ovulation and fertilisation of the oocyte (Ojeda *et al*, 1982; Hizaki *et al*, 1999), doing so via four G-coupled protein receptors (GPCRs), EP1-4. Each of these signals via a different downstream pathway; EP1 signals via Gq to up-regulate intracellular calcium; EP2 and EP4 are ‘stimulatory’ receptors and signal via G_s to increase cyclic adenosine monophosphate (cAMP), with EP4 also able to act via the PI3/AKT pathway; and EP3 is regarded as ‘inhibitory’ and signals via G_i to decrease cAMP (Alfranca *et al*, 2006) (Figure 1.9). This variance in downstream signalling, coupled with varying localisation to different cell types, allows a single prostanoid to exert multiple functions in a single tissue.

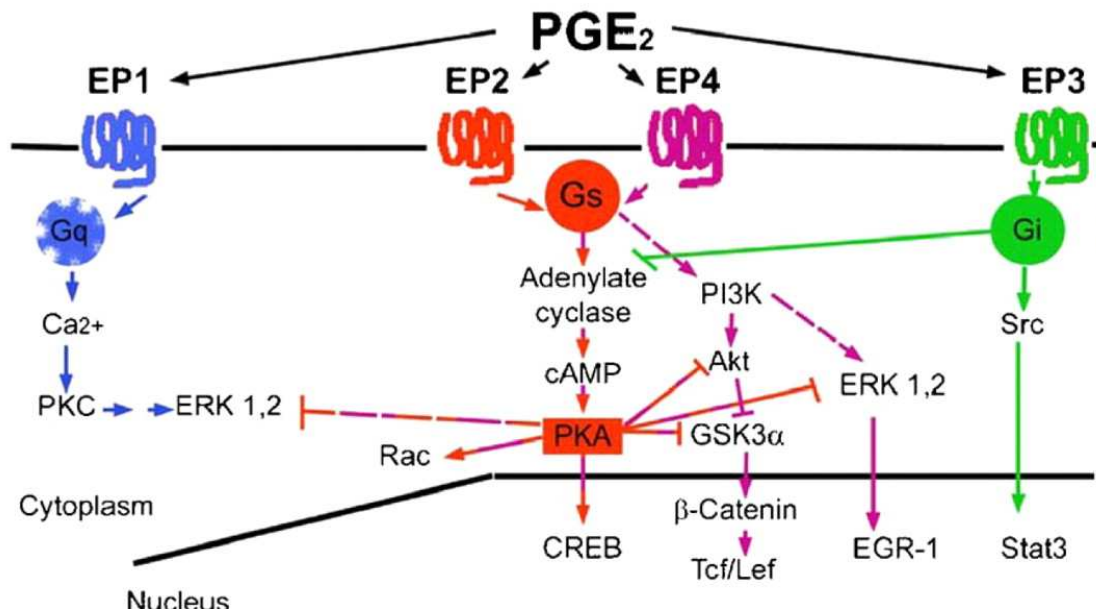


Figure 1.9 Specific downstream signalling of the four EP receptors

PGE₂ is able to signal via 4 G-coupled protein receptors (EP1-4), each of which signals via a distinct downstream intracellular cascade. EP1 signals via Gq to increase intracellular calcium, EP2 and EP4 via G_s to induce adenylate cyclase activity (with EP4 also inducing the PI3K/AKT pathway), and EP3 via G_i inhibits adenylate cyclase activity and induces Stat signalling. Figure adapted from (Alfranca *et al*, 2006).

In addition to classical ligand receptor action, there is also evidence that the EP receptors can be internalised to the nucleus to directly regulate gene transcription (Bhattacharya *et al*, 1998; Bhattacharya *et al*, 1999; Desai *et al*, 2000). Of the EP receptors, EP2 is thought to be the most involved in ovarian function, determined by the ovulatory defects and failure of fertilisation in *Ep2* homozygous null mice, whereas inactivation of the remaining Ep receptors lead to no major reproductive dysfunction (Hizaki *et al*, 1999; Kennedy *et al*, 1999; Tilley *et al*, 1999). It was determined that gonadotropins increase both *Cox2* and *Ep2* levels in the adult ovary leading to cumulus expansion (Hizaki *et al*, 1999), which is sustained by the positive feedback capabilities of the PGE₂ system. It is likely the *Ep2*^{-/-} phenotype may be a result of inhibition of this signalling pathway.

Apart from reproductive function, PGE₂ mediates development of other organs, most critically closure of the ductus arteriosus, which allows for postnatal circulation, and is the main cause of fatality in *COX1/2*^{-/-} doubly ablated mice (Nguyen *et al*, 1997; Loftin *et al*, 2001). PGE₂ regulation of fetal angiogenesis is also well characterised (Majima *et al*, 1997), and is likely to be mediated by the angiogenic factors up-regulated by PGE₂ including bFGF and vascular endothelial growth factor (VEGF) (Cheng *et al*, 1998). Additionally, PGE₂ is postulated to be required for blastocyst development (Dey *et al*, 1980; Davis *et al*, 1983), as inhibition of the COX enzymes during pregnancy results in degradation of murine blastocysts (Cha *et al*, 2006). This key role in development is also noted in the inhibition of PGE₂ in the zebrafish, where it regulates cell migration necessary for gastrulation (Cha *et al*, 2006).

With roles in both the adult ovary and development of other organ systems, PGE₂ is an attractive candidate for possible regulation of fetal ovarian development. PGE₂ has also been shown to interact with established germ cell niche factors. PGE₂ is known to be up-regulated during human placental development, when the hypoxic environment activates Activin A (Petraglia *et al*, 1993; Jenkin *et al*, 2001; Supramaniam *et al*, 2004), it is also demonstrated to regulate *BMP2*, 4, and 7 in osteoid cells (Virdi *et al*, 1998; Takiguchi *et al*, 1999; Paralkar *et al*, 2002), and induces *BDNF* expression in astrocytes (Toyomoto *et al*, 2004; Hutchinson *et al*, 2009). In addition, an recent exploratory gene expression assay revealed PGE₂ as a

potent regulator of the neurotrophins in female reproductive tissues (Jabbour, unpublished). However, none of these interactions/relationships have been confirmed in the human fetal ovarian environment.

1.9.2 The IL6-type cytokines

The IL6-type cytokines are secreted, pro/anti-inflammatory cytokines which demonstrate overlapping function and may, like PGE₂, be involved in fetal ovarian development. The IL6-type cytokine family is composed of several cytokines which signal via receptor complexes consisting of shared components, and includes IL6, IL11, leukaemia inhibitory factor (LIF), oncostatin-M (OSM), cardiotropin-1 and ciliary neurotrophic factor (CNTF) (Heinrich *et al*, 1998). The IL-6 type cytokines signal via receptor complexes made up of hetero- or homo- dimers or trimers, with a common receptor component gp130 in each receptor complex (Figure 1.10). As reviewed in detail (Heinrich *et al*, 1998); each receptor complex contains one or more shared signal transducing components, and some complexes also include an α -receptor subunit, which although not required for intracellular signalling is necessary for specific ligand binding. LIF and OSM share the same signalling complex consisting of a heterodimer of LIF receptor (LIFR) and gp130 (Gearing & Bruce, 1992). OSM is also able to signal via a heterodimer of a newly characterised OSM receptor (OSMR) and gp130 (Ichihara *et al*, 1997). Comparable to LIF and OSM, CNTF also utilises the LIFR/gp130 heterodimer, but also requires a specific CNTF receptor (CNTFR) α subunit for signalling (Gearing & Bruce, 1992; Davis *et al*, 1993). Finally, IL6 ligand utilises an α -receptor subunit, IL6 receptor in combination with a homodimer of gp130 (IL6R) (Taga *et al*, 1989). Several studies have demonstrated a high degree of redundancy in IL6-type cytokine function as a result of shared receptor components and similar intracellular signalling (Koshimizu *et al*, 1996; Liu *et al*, 2000).

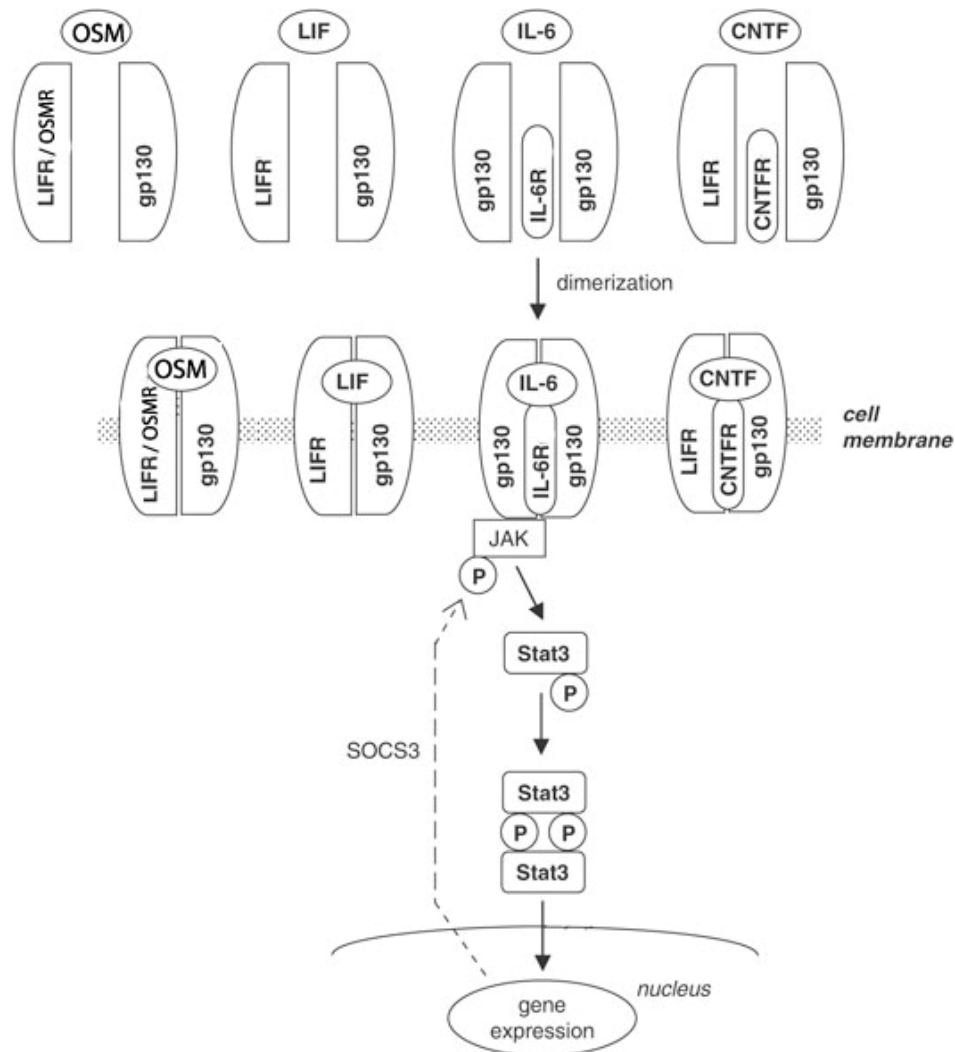


Figure 1.10 IL6-type cytokine signalling

As described fully in the text, the IL6 type cytokines signal via formation of hetero- or homo- dimers or trimers of various shared receptor components to intracellularly signal via the Jak/STAT pathway in order to modulate gene expression. This signalling can be inhibited via SOCS3, which is also a downstream target of IL6-type signalling and thus part of a negative feedback loop. Figure adapted from (Suzuki *et al*, 2009).

The IL6-type cytokine receptor complexes signal via activation of the Janus kinases (Jaks) and the signal transducer and activator of transcription (STAT) transcription factor (Jak/STAT) pathway (Lutticken *et al*, 1994; Stahl *et al*, 1994). The activation of this signalling pathway via various phosphorylation events is able to regulate target gene expression via phosphorylated dimerisation of STATs which is required for DNA binding (Shual *et al*, 1993). However, Jak/STAT regulation is known to be transient and thus effective mediators of the system, specifically suppressors of cytokine signalling 3 (SOCS3), have been identified (Nicholson *et al*, 2000; Schmitz *et al*, 2000). STAT dimers are able to up-regulate various transcripts, including the SOCS inhibitory factors themselves (Heinrich *et al*, 1998), which in turn act as negative feedback inhibitors by acting on activated IL6 receptors or Jaks to inhibit further signalling. Both IL6 and LIF signalling are known to induce SOCS3 expression, suggesting these factors are able to promote their own negative feedback loop, limiting signalling and allowing for acute regulation (Endo *et al*, 1997). This acute regulation allows the IL6-type cytokines to regulate specific events in various tissues, including the ovary. In the adult ovary, IL6-type cytokines are involved in various processes including cumulus expansion and oocyte competence (Liu *et al*, 2009).

As with Oct4 and Nanog, the IL-6 type cytokine family was originally highlighted as a potential regulator of germ cell development based upon various *in vitro* experiments using stem cells, embryonic germ (EG) cells, and PGCs (Williams *et al*, 1988; Defelici & Dolci, 1991; Matsui *et al*, 1991; Resnick *et al*, 1992; Cheng *et al*, 1994; Koshimizu *et al*, 1996). LIF ligand in particular has been well characterised in the maintenance of ES cells and PGCs in culture in combination with KITL and bFGF (Matsui *et al*, 1991; Resnick *et al*, 1992), thus demonstrating regulation of proliferation and survival. Further studies demonstrated LIF function could be replicated by addition of IL6, CNTF or OSM to the culture media, demonstrating compensatory action (Cheng *et al*, 1994; Koshimizu *et al*, 1996). Further, culture of mouse PGCs demonstrated reduction in apoptosis with LIF treatment (Pesce *et al*, 1993a), and that the common signalling component gp130 is able to regulate initiation of meiosis (Chuma & Nakatsuji, 2001). Based upon this accumulation of

in vitro data, it was hypothesised the IL6-type cytokines had a role in germ cell function *in vivo*, specifically during early development and maturation.

However, as discussed for both Oct4 and Nanog, regulatory roles demonstrated in ES cells and/or PGCs *in vitro* often differ from their physiological roles *in vivo*. To date, several genetically engineered murine models have been generated in attempts to recapitulate the regulation of IL6-type cytokines seen *in vitro* in the fetal gonad (Stewart *et al*, 1992; Escary *et al*, 1993; Ware *et al*, 1995; Yoshida *et al*, 1996; Molyneaux *et al*, 2003a) with little success. Systemic deletion of LIF was the first model to be investigated, which did result in infertility in female offspring, but it was identified this was the result of an ovulatory defect rather than an effect on germ cell differentiation (Stewart *et al*, 1992). As the IL6-type cytokines are known to have overlapping function, several models focused on shared signalling components, in order to prevent compensation by other IL6 cytokines which might mask function (Ware *et al*, 1995; Yoshida *et al*, 1996; Takeda *et al*, 1997). However, homozygous deletion of the shared receptor components gp130 or LIFR or the common downstream target *STAT3* resulted in a lethal phenotype, either embryonically or shortly after birth (Ware *et al*, 1995; Yoshida *et al*, 1996; Takeda *et al*, 1997), preventing any elucidation of systemic blockage of IL6-type cytokine signalling. A *gp130* germ cell specific knockout was also generated utilising the *TNAP*-CRE, as previously described for Oct4 and Nanog (Molyneaux *et al*, 2003a). This line resulted in no change in ovarian phenotype during fetal and early postnatal life (although there was an ovulation defect in adult female and a reduction in PGCs in male pups (Molyneaux *et al*, 2003a).

Although several attempts have been made to elucidate IL6-type cytokine function *in vivo*, their role during fetal gonad development has not been established. In addition little is known about the IL6-type cytokines and their receptors in the human fetal ovary, despite strong evidence for these factors as regulators of differentiation and proliferation *in vitro*. For these reasons, the IL6-type cytokines were hypothesised to function as part of the germ cell niche during ovarian development.

1.9.3 The Prokineticins

A final group of regulators were also hypothesised to regulate fetal ovarian development; the prokineticins (PROK) 1 and 2, which are recently described proteins known to regulate angiogenesis and inflammation (Catalano *et al*, 2010; Monnier & Samson, 2010). The name prokineticin reflects how the proteins were originally characterised, as potent regulators of smooth muscle contractility in the gastrointestinal tract (Li *et al*, 2001) (eg. pro- kinetic). The PROKs have similar function to vascular endothelial growth factor (VEGF) in promotion of angiogenesis, and PROK1 was initially termed endocrine gland VEGF (EG-VEGF) (LeCouter *et al*, 2001). In addition, PROK1 was also named venom protein A (VPRA) and mamba intestinal toxin1 (MIT1), as the PROK1 orthologue was initially identified as a non-toxic protein derived from the venom of the black mamba snake (*Dendroaspis polylepis*) (Joubert, 1980; Schweitz *et al*, 1990). PROK2 was also identified in a different species by a different name; Bv8, derived from the skin secretions of the yellow-bellied toad (*Bombina variegata*) (Mollay *et al*, 1999). Despite various aliases and nomenclatures, the human orthologues of the PROKs were identified and termed PROK1 and PROK2, as they will be referred to in this report.

The PROKs signal via two prokineticin receptors (PROKR1 and PROKR2) (Masuda *et al*, 2002) which share 87% homology (Soga *et al*, 2002). Both PROK ligands are able to signal interchangeably via the two GPCRs; however, PROK2 has a slightly higher affinity for both receptors (Lin *et al*, 2002; Soga *et al*, 2002). The PROKRs then signal via either Gi or Gq signalling, which in turn increases intracellular calcium concentration and provokes rapid activation of p44/p42 MAP kinase signalling as well as activation of STAT signalling (Lin *et al*, 2002; Masuda *et al*, 2002; Soga *et al*, 2002).

Although initially characterised in endothelial cells, PROK receptors and ligands are expressed in various cell types throughout the body. PROK1 is expressed in B and T cells (Dorsch *et al*, 2005) and PROK2 in bone marrow, blood cells, immune cells, and neuronal tissue (LeCouter *et al*, 2004). In these systems PROKs are shown to promote proliferation, differentiation and survival (Melchiorri *et al*, 2001; LeCouter *et al*, 2004). Additionally, both ligands are highly expressed in the steroidogenic

reproductive tissues, such as the gonads (Wechselberger *et al*, 1999; Ferrara *et al*, 2003; Kisliouk *et al*, 2003; LeCouter *et al*, 2003; Samson *et al*, 2004), the placenta (LeCouter *et al*, 2001; Hoffmann *et al*, 2006) the endometrium (Evans *et al*, 2008; Evans *et al*, 2009) and the adrenal glands (Lin *et al*, 2002). Although relatively little systemic data is available for these recently characterised proteins, each ligand has been well characterised in a distinct organ system. PROK1, as alluded to previously, is extensively described in its role in smooth muscle contractility, with evidence for regulation of most of the GI tract in various species (Li *et al*, 2001; Hoogerwerf, 2006; Wade *et al*, 2010). However this role is not shared with PROK2, which demonstrates that, although similar, the two ligands share distinct roles in different systems (Bassil *et al*, 2005). PROK1 and 2 are able to induce proliferation and differentiation in the central nervous system (CNS) (Ngan *et al*, 2007; Ngan *et al*, 2008; Ruiz-Ferrer *et al*, 2011), but only PROK2 is able to regulate more specific CNS processes such as circadian rhythm, pain sensation, appetite, locomotor activity and thermoregulation (Cheng *et al*, 2002; Negri *et al*, 2002; Cheng *et al*, 2005; Prosser *et al*, 2007; Jethwa *et al*, 2008; Ren *et al*, 2011).

Despite the elucidation of PROK function in other organ systems, little is known their roles in the gonads, despite being localised in the interstitial cells of both the testis and ovary (Wechselberger *et al*, 1999; Ferrara *et al*, 2003; Kisliouk *et al*, 2003; LeCouter *et al*, 2003; Samson *et al*, 2004). Homozygous ablation of *Prok2* or *Prokr2* using rodent models resulted in the atrophy of the reproductive system (male or female) similar to the phenotype seen in human Kallmann syndrome (Dode *et al*, 2006; Matsumoto *et al*, 2006; Pitteloud *et al*, 2007); however it was determined this was likely due to *Prok2/Prokr2* effects on gonadotropin-releasing hormone (GnRH) expression, rather than direct regulation in the gonads (Matsumoto *et al*, 2006; Pitteloud *et al*, 2007). Further evidence of this regulation was found in women who suffer reversible hypothalamic amenorrhea (predisposition to GnRH deficiency/disruption after exposed to stressors), which found several of these women had mutations in PROKR2 (Caronia *et al*, 2011). Although not yet defined, it has been postulated PROK1 does have a direct role in the ovary and is localised to the theca cells in adult tissues (Ferrara *et al*, 2003; Kisliouk *et al*, 2003). This

hypothesis is based upon the observation that PROK1 transcript expression increases with development of the corpus luteum (Ferrara *et al*, 2003; Fraser *et al*, 2005). However, further mechanistic investigation and localisation of the PROK receptors has yet to be performed.

However, two recent transcriptome studies have demonstrated the *PROKs* are expressed and may play a role in the fetal ovary. One array demonstrated increased expression of *Prok1* in the fetal ovary comparative to the fetal testis (Houmard *et al*, 2009). The other detected novel expression of *PROK2* in the human fetal ovary which increased with gestation leading to primordial follicle formation, suggesting a possible role for the ligand in ovarian development (Fowler *et al*, 2009). Further, there is evidence from other reproductive tissues, that the *PROKs* may regulate signalling components of the other candidate regulators (PGE₂ and the IL6-type cytokines) (Denison *et al*, 2008; Evans *et al*, 2008; Evans *et al*, 2009; Cook *et al*, 2010).

In addition to the hypothesis that the *PROKs* may be active in regulating the human fetal ovary, it is also postulated the *PROKs* may play a role in fetal testis development, as several studies have highlighted increased expression of *PROK2* and *PROKR2* in the fetal testis compared to both the fetal ovary, and other tissues, including the brain where *PROK2* and *PROKR2* are known to be highly active (Wechselberger *et al*, 1999; LeCouter *et al*, 2003; Samson *et al*, 2004). These studies also highlighted a potential role for *PROK* regulation of steroidogenesis, which is integral to sex differentiation and further testis development. With this data in mind, the expression of *PROKs* in the human fetal ovary and testis were further characterised, to explore both *PROK* regulation during fetal gonad development, but also differential regulation between the sexes.

1.10 Aims of PhD

Human fetal ovarian development is critical, as primordial follicle development at this stage underpins adult fertility in later life. The fetal ovary and germ cells within are regulated by the germ cell niche, which regulates progression from PGC specification to primordial follicle formation. Despite the importance of the germ cell niche, few of its contributing factors have been identified, leaving the regulation of early ovarian development poorly understood. It is likely the germ cell niche is more similar to a web than a single cascade, allowing for positive and negative feedback loops/checks and balances in the system to prevent disruption. Therefore, the question remains: What factors make up the germ cell niche, and how do these factors interact to regulate fetal ovarian development?

In order to further answer this question, several factors implicated in regulation of reproductive function later in life, which were known to interact with established factors of the germ cell niche were identified; PGE₂, the IL-6 type cytokines, and the PROKs. It was postulated that these regulatory factors (or families of factors), were involved in fetal ovarian development and primordial follicle formation.

The specific aims of this research were to:

1. Examine expression and localisation of signalling PGE₂ components across human gestation (8-20 weeks), and further investigate transcriptional and functional effects of PGE₂ treatment *ex vivo* in human fetal ovarian samples.
2. Further determine the relationship between PGE₂ signalling and germ cell development *in vivo*, utilizing a fetal rat model of COX inhibition via paracetamol exposure.
3. Explore the roles of the IL6-type cytokines in the human fetal ovary to further clarify *in vivo* roles during germ cell development, and to further clarify if regulation seen in ESC culture *in vitro* is relevant to PGCs and oocytes *in vivo*.

4. Characterise PROK expression and localisation in the human fetal ovary, and further investigate function via the creation of a germ cell line stably expressing PROKR1, to determine signalling pathways regulated by PROK1-PROKR1 interaction.

Secondary to the focus on the ovarian germ cell niche is interest in how ovarian and testicular development differ, and how the same regulatory factors have differing roles in the two systems. As the PROKs are differentially expressed in the testis and the ovary in both the human and the mouse, it was hypothesised that PROKs might have differing regulation in each system, and thus were also investigated in the fetal testis:

5. Compare PROK expression and localisation in the human fetal testis to that demonstrated in the human fetal ovary, and further identify sex-specific function by culturing interstitial cells isolated from human fetal testes.

Chapter 2

General Materials and Methods

Chapter 2. General Materials and Methods

2.1 Human Dissection and Tissue Collection

Human fetuses (8-20 wks) were obtained as previously described in (Coutts *et al*, 2008). Informed consent was given, and the study approved by the Lothian Research Ethics Committee (LRC08/S1101/1). Surgical terminations were also obtained after administration of misoprostol (200mg per vaginam) via vacuum aspiration. General aesthetic was used during the procedure.

It is recognised misoprostol treatment may interfere with parts of this study that focus on prostaglandin interaction in fetal tissue. However, as tissue collected responded to PGE₂ treatment, it is unlikely that the gonads are greatly affected by maternal misoprostol treatment (see Chapter 3).

All fetuses were gestationally aged based on ultrasound scan. This gives an 'obstetric' gestation based on last menstrual period rather than post-conception dating. After the specimens were obtained this gestation was confirmed utilising either crown-rump length in first trimester specimens or foot length in second trimester specimens.

After obtaining samples, tissue was transported to the laboratory for further dissection. Micro-dissection to remove the gonads was performed in sterile conditions and further tissue taken for SRY polymerase chain reaction (PCR) as explained below (Section 2.3) in order to sex first trimester fetal gonads. Gonads to be used for RNA/protein analysis or tissue culture were carefully separated from all extraneous material including the mesonephros using sterile needles (BD).

2.2 Rat Treatment, Dissection and Tissue Collection

Female Wister rats were maintained according to UK Home Office guidelines and fed soy-free breeding diet (RM3 (E) soya free, SDS). Rats were kept in controlled lighting housing (on at 0700h, off at 1900h) at a temperature of 19-21° C with LITASPEN standard bedding (SPPS). Timed matings were established by visible vaginal plug and deemed embryonic day (e) 0.5. At e13.5 of gestation, dams were fed via gavage 350 mg/kg paracetamol (Sigma) diluted in corn oil (Mazola). A dosage of 350 mg/kg paracetamol was utilised as previous studies had determined this concentration was high enough to affect rodent fetuses without causing maternal morbidity (including liver necrosis) (Kristensen *et al*, 2011). A higher dosage than that which a pregnant woman would use was utilised as rats have both an increased basal metabolic rate (~7x that of the human) and drug clearance rate (acetaminophen/paracetamol ~8.6x that of the human) comparative to humans (Choiu *et al*, 1998). Gavage delivery of paracetamol was utilised to mimic oral delivery of paracetamol in humans, with one large bolus rather than multiple doses to reduce stress to the animals which may have obscured effects of the drug itself.

Control dams received corn oil via gavage only. This was repeated every morning for 7 days (e20.5), followed by culling of the dams via cervical dislocation at e21.5. Pups were recovered and weighed before being culled via decapitation. Ovaries were removed via micro-dissection and one was snap frozen at -80° C for further analysis via enzyme linked immunosorbent assay (ELISA), while the other was fixed in Bouins solution (Clintech) for 1 h and processed as described in section 2.6.

2.3 SRY Genotyping

PCR amplification of the sex-determination gene (*SRY*) was performed to determine the sex of human first trimester specimens, as gender cannot be visually determined (Friel *et al*, 2002). The sample of specimen retained for DNA extraction was added to 100 µl of 25 mM NaOH/0.2 mM EDTA. The solution was heated at 95° C for 20 min and then neutralised in 100 µl of 40 mM Tris.HCl on ice.

The samples are vortexed for 1 min and 5 µl of the sample added to the reaction mix (Table 2.1). Remaining sample can be stored at -20°C.

Table 2.1 SRY RT-PCR Reaction Mix

Reagent	Amount Used	Manufacturer
ImmoMix Red	12.5 µl	Bioline
25 µM SRY Forward Primer	0.5 µl	Eurogentech
25 µM SRY Reverse Primer	0.5 µl	Eurogentech
H ₂ O	6.5 µl	Ambion

The reaction mix was run on a thermocycler (PTC-100, MJ Research Inc) as in Table 2.2. Each sample was run with a 100 bp ladder (Promega) via electrophoresis on a 1% agarose gel (Sigma) containing Gel Red (Biotium) for visualisation. A product of 300 bp confirms the specimen as male, absence of the band is determined as female. Known positive and negative controls were utilised to ensure reaction success.

Table 2.2 SRY PCR Thermocycler Programme

Step	Temperature	Time
1	95°C	10 min
2	95°C	30 sec
3	58°C	30 sec
4	72°C	45 sec
Repeat steps 2-4 for 35 cycles		
5	72°C	10 min

2.4 cDNA synthesis and RT-PCR

Snap frozen samples (-80° C) were homogenised and RNA extracted using the RNeasy Micro Kit (Qiagen) with on-column DNase digestion according to manufacturer's instructions. Reverse transcription was performed using the Superscript VILO kit (Invitrogen) according the manufacturer's instructions, 0.5 µg of RNA was used in each reaction. Negative control samples (RT-) lacking transcription enzyme were also synthesised to identify contamination in further experiments.

Target-specific PCR was performed to determine presence or absence of specific transcripts using 1 µl of the RT+ or RT- cDNA reaction in a reaction volume of 25 µl (Table 2.3). Products were run on agarose gels (1-2.5%, Sigma) with a 100 bp ladder (Promega) using electrophoresis. Primer pairs can be found in Table 2.4.

Table 2.3 RT-PCR Reaction Mix

Reagent	Amount Used	Manufacturer
ImmoMix Red	12.5 µl	Bioline
25 µM Forward Primer	0.5 µl	Eurogentech
25 µM Reverse Primer	0.5 µl	Eurogentech
H ₂ O	10.5 µl	Ambion

Table 2.4 PCR Primer Pairs

Gene Target	Forward Primer	Reverse Primer	Product Size
3 β -HSD	GCGGCTAATGGGTGGAATCTA	CTGGCAGAAAGGAATGGGCC	101 bp
AMH	ACATCAGGCCCAGCTCTATCAC	TGTTTGTGCAGGACAGACCC	151 bp
BDNF	AACAATAAGGACGCAGACTT	TGCAGTCTTTTTGTCTGCCG	222 bp
CNTF	CAGGGCCTGAACAAGAACAT	CTAAGAGCCTGGCCAACAAA	151 bp
COX-1	TGTTCTGGTGTCCAGTTCCAATA	ACCTTGAAGGAGTCAGGCATGAG	95 bp
COX-2	CCTTCCTCCTGTGCCTGATG	ACAATCTCATTTGAATCAGGAAGCT	82 bp
CYP11A1	CCAGACCTGTTCCGTCTGTT	GAAGTTCTGGGTGTATATGTCAGC	99 bp
DAZL	GAAGGCAAAATCATGCCAAACAC	CTTCTGCACATCCACGTCATTA	186 bp
DESMIN	GGAGATTGCCACCTACCG	GGTCTGGATGGGGAGATTG	67 bp
DKK1	GCGGGAATAAGTACCAGACCAT	GGGACTAGCGCAGTACTCATCAGT	92 bp
EP1	AGATGGTGGGCCAGCTTGT	GCCACCAACACCAGCATTG	73 bp
EP2	GACCGCTTACCTGCAGCTGTAC	TGAAGTTGCAGGCGAGCA	71 bp
EP3	GACGGCCATTACAGCTTATGG	TTGAAGATCATTTTCAACATCATTATCA	87 bp
EP4	ACGCCGCCTACTCCTACATG	AGAGGACGGTGGCGAGAAT	64 bp
GAPDH	GACATCAAGAAGGTGGTGAAGC	GTCCACCACCCTGTTGCTGTAG	212 bp
GP130	CTGAATGGGCAACACACAAGTT	CCAGACTTCAATGTTGACAAAATACA	107 bp
ID3	CTCTTCAGGCCACAAGTTCAC	GTGTCCTGACACCTCCAGAAC	192 bp
IL6	GCCGCCCCACACAGACA	CCGTCGAGGATGTACCGAAT	71 bp
IL6R	AGCTCAGATATCGGGCTGAA	GGACTCCTGGATTCTGTCCA	202 bp
INHBA	GGCAAGTTGCTGGATTATAGTG	CCACATACCCGTTCTCCCCGAC	272bp
LIF	TGGTGGAGCTGTACCGCATA	TGGTCCCGGGTGATGTTG	64 bp
LIFR	TCAAAGGGGCCTGATACTTG	CTGCTTTGTGCTGAGGATCA	178 bp
MCL1	ATCTCTCGGTACCTTCGGGAGC	GCTGAAAACATGGATCATCACTCG	221 bp
NTF5	QUANTITECT PRIMAR Assay Hs_NTF5_1_SG (QIAGEN)		96 bp
OCT4	ACATCAAAGCTCTGCAGAAAGAAC	CTGAATACCTTCCCAAATAGAACCC	126 bp
OSM	ACAGAGGACGCTGCTCAGTC	AGGAGTCTGCTGGTGTCTCTG	150 bp
OSMR	TTGACAACCCGGAAGAAAAG	TGAATCAGCATCGAGGAGTG	157 bp
PROK1	GTGCCACCCCGGCAG	AGCAAGGACAGGTGTGGTGC	65 bp
PROKR1	TCTTACAATGGCGGTAAGTCCA	CTCTTCGGTGGCAGGCAT	69 bp
PROK2	TTGGGCGGAGGATGCA	AAATGAAGTCCGTAAACAGGCC	65 bp
PROKR2	GCTCTGTGCCTCCGTCAACT	CCAGCAAGGCATTGGTGG	65 bp
PTGES	GAAGAAGGCCTTTGCCAAC	GGGTTAGGACCCAGAAAGGA	168 bp
RPL32	CATCTCCTTCTCGGCATCA	AACCCTGTTGTCAATGCCTC	100 bp
SMAD2	TTTCAGTTCCGCCTCCAATCGC	CGTGAATGGCAAGATGGACG	208 bp
SMAD3	TGAGGCTGTCTACCAGTTGACC	CTAAGACACACTGGAACAGCGG	199 bp
StAR	GGCATCCTTAGCAACCAAGA	ACTTTGTCCCCATTGTCCTG	62 bp
VASA	AAGAGAGGCGGCTATCGAGATGGA	CGTTCACCTCCACTGCCACTTCTG	238 bp

2.5 Quantitative RT- PCR

Quantitative real time PCR (qRT-PCR) was performed to determine mRNA transcript levels using Applied Biosystems 7500Fast or 7900Fast instruments (specified in each chapter). Standard curves for all targets were performed as described (Coutts *et al*, 2008) using either late second trimester fetal ovarian or endometrial cDNA to ensure proper reaction efficiency was achieved for each target. All measurements were performed in duplicate 10 µl reactions.

For relative comparison, PowerSYBR Green Master Mix (ABI) was utilised and targets were analysed alongside a ubiquitously expressed ‘housekeeping’ gene (*GAPDH* or *RPL32*) and calculated as relative expression. Each reaction was performed in a single well of a 96-well reaction plate (Applied Biosystems) as described in Table 2.5.

Table 2.5 Sybr Green Reaction Mix

Reagent	Amount Used	Manufacturer
Sybr Green	5 µl	Invitrogen
25 µM Forward Primer	0.2 µl	Eurogentech
25 µM Reverse Primer	0.2 µl	Eurogentech
H ₂ O	3.6 µl	Ambion
Sample (diluted 1/10 in H ₂ O)	1 µl	--

Some primers were designed and donated by the Henry Jabbour lab for Taqman multiplexing comparison using Express qPCR Super Mix with Premixed ROX (Invitrogen) (targets used in this manner are listed in Table 2.8). Similarly, some primers were designed and donated by the Philippa Saunders lab and utilised for multiplexing comparison using the Universal Probe Library (Roche). These primers alongside specifically designed probes were utilised with internal-well comparison marker 18s (ribosomal RNA control, Applied Biosystems). Each target was calculated and presented as relative expression to this internal control in a reaction mixes are as described in Table 2.6 and 2.7.

Table 2.6 Taqman Reaction Mix

Reagent	Amount Used	Manufacturer
Super Mix	6.3 µl	Invitrogen
25 µM Forward Primer	0.2 µl	Eurogentech
25 µM Reverse Primer	0.2 µl	Eurogentech
5 µM Probe	0.5 µl	Eurogentech
18s	0.2 µl	Applied Biosystems
H ₂ O	4.6	Ambion
Sample (diluted 1/10 in H ₂ O)	1 µl	--

Table 2.7 Universal Probe Taqman Reaction Mix

Reagent	Amount Used	Manufacturer
Super Mix	7.5 µl	Invitrogen
200 nM Forward Primer	0.15 µl	Eurogentech
200 nM Reverse Primer	0.15 µl	Eurogentech
100 nM Universal Probe	0.15 µl	Roche
18s	0.1125 µl	Applied Biosystems
H ₂ O	5.4375 µl	Ambion
Sample (diluted 1/10 in H ₂ O)	1.5 µl	--

Table 2.8 PCR Probes

Gene Target	Probe
CYP11A1	Universal Probe Library (Roche) – Probe 11
DESMIN	Universal Probe Library (Roche) - Probe 55
DKK1	TACCAGCCGTACCCGTGCGCAG
PROKR1	TGCAGACCTGGACCTCAAGACAATTGG
PROK2	CACTTGCCCATGTCTGCCAGGCT
PROKR2	CCTGCGCACCGTCTCCCTCTACG
StAR	Universal Probe Library (Roche) – Probe 11

Data analysis was performed using GraphPad Prism version 5 (GraphPad Software Inc). One-way ANOVA and t-tests were performed with post-testing as described for each chapter.

2.6 Tissue Fixation, Processing, and Slide Prep

Tissue was fixed in Bouins solution (Clintec) for 2-3 hours and then transferred to 70% ethanol (VWR) for immunohistochemistry.

Fixed tissue was processed in an automated Leica TP1050 processor and embedded in paraffin wax. Paraffin blocks were cut via microtome into 5 µm thick sections and floated in a warm water bath to promote smooth tissue transfer. Sections were mounted on electrostatically charged glass slides (pink slides for human tissue, Thermo-scientific; white slides for animal tissue, Leica). The slides were kept at 50°C overnight in a slide oven to ensure tissue adhered to the slide surface.

2.7 Haematoxylin and Eosin Staining

2.7.1 Dewaxing and Rehydration

Samples from each specimen were taken every 10th slide to determine tissue quality and orientation. Slides were dewaxed and rehydrated through a series of alcohol gradients. The slides are first put in xylene (VWR) twice for 5 min, then moved to absolute alcohol twice for 20 sec, 90% alcohol for 20 sec, 80% alcohol for 20 sec, 70% alcohol for 20 sec, and finally in tap water.

2.7.2 Counterstaining

Slides were immersed in haematoxylin (Leica), a blue nuclear counterstain, for 30-60 sec. Slides were washed in water to remove excess stain and immersed in acid alcohol (section 2.13) to remove non-specific cytoplasmic staining. Slides were rinsed again in water to remove the acid alcohol and further immersed in Scott's tap water (section 2.13) for 30 sec to allow the haematoxylin to develop. Slides were then immersed in Eosin, (BD) a red cytoplasmic stain, for 1 min, and rinsed in tap water.

2.7.3 Dehydration and Mounting

After counterstaining the slides were dehydrated in preparation for mounting. This is done by immersing the slides in 70% ethanol for 20 sec, 85% ethanol for 20 sec, 95% ethanol for 20 sec, and finally 100% ethanol twice for 20 sec each. The slides were then immersed in xylene twice for 5 min.

After dehydration the slides are mounted using glass coverslips (VWR) and Pertex (Histolab), mounting solvent based glue. Air pockets were pushed away from the tissue section with pressure applied by forceps, and the slides left to dry. The slides were analysed as described below and stored in dry storage at room temperature.

2.8 Immunohistochemistry

Immunohistochemistry was used to for localisation and visualisation of target proteins in tissues of interest.

2.8.1 Dewaxing and Rehydration

Dewaxing and rehydration were performed as described above, moving the slides to antigen retrieval after the first series of alcohol immersions.

2.8.2 Antigen Retrieval

In order to ensure detection of proteins that may have been masked during the fixation process, the tissue is exposed to high temperature and pH change (Shi *et al*, 1993). Antigen retrieval was performed in 0.01 M citrate buffer with a pH of 6.0 in a standard domestic pressure cooker. The slides were added to 2000 ml of boiling citrate buffer (section 2.13) and the pressure cooker sealed for 5 min. The pressure cooker was then taken off the heat source and the pressure released. The slides were left to stand for 20 min, after which they were cooled with water.

2.8.3 Non-Specific Blocking

To prevent non-specific detection by the primary or secondary antibody, the slides are blocked using peroxide blocking solution (section 2.13) rocking for 30 min (all rocking is performed at 20-40 rpm). The slides are then washed in tris buffered saline (TBS) twice for five min.

After peroxidase blocking, the slides are blocked for endogenous biotin, which is known to be prevalent in human tissue. This is done via a streptavidin/biotin blocking kit (Vector). The streptavidin solution is applied neat to the tissue for 15 min incubation in a humidity chamber, and then the slides are washed in TBS twice for five min. The biotin solution is applied as previously described for the streptavidin solution and the slides washed after incubation.

To further prevent non-specific binding of the secondary antibody, the slides are incubated for 30 min in a blocking buffer consisting of normal serum (NS)(Biosera) diluted in TBS (1:4) containing 5% bovine serum albumin (NS/TBS/BSA) in a humidity chamber. Normal goat serum (NGS) was used unless the primary antibody was raised in goat, in which case normal rabbit serum was used in the blocking buffer.

2.8.4 Primary Antibody

The blocking serum (NS/TBS/BSA) was then replaced with primary antibody diluted in blocking serum to an optimised concentration. Concentration was determined for each antibody by titering the dilution of the antibody on standard tissue to find the maximum level of detection lacking non-specific background staining. The primary antibody is left on the tissue overnight at 4° C. The table below (Table 2.9) describes the antibodies used and optimum concentrations for fetal tissue.

Appropriate negative and positive controls were included as appropriate. Negative controls were done in two ways (as outlined in each chapter); adding no primary antibody to the serum for the overnight incubation, or adding antibody that was incubated with peptide to block binding and reveal any non-specific binding that may have occurred.

Table 2.9 Antibodies used for Immunohistochemistry

Primary Antibody	Dilution	Species Raised	Secondary	Manufacturer
BrdU	1:1000	Sheep	Rabbit Anti-Sheep	Fitzgerald
COX1	1:50	Goat	Rabbit Anti-Goat	Santa Cruz
COX2	1:50	Goat	Rabbit Anti-Goat	Santa Cruz
CC3	1:75	Rabbit	Rabbit Anti-Goat	Cell Signaling
EP1	1:700	Rabbit	Goat Anti-Rabbit	Cayman
EP2	1:100	Rabbit	Goat Anti-Rabbit	Cayman
EP3	1:2000	Rabbit	Goat Anti-Rabbit	Cayman
EP4	1:250	Rabbit	Goat Anti-Rabbit	Cayman
GP130	1:1000	Rabbit	Goat Anti-Rabbit	Santa Cruz
LIFR	1:100	Rabbit	Goat Anti-Rabbit	Santa Cruz
PHH3	1:3000	Rabbit	Goat Anti-Rabbit	Upstate
PROK1	1:250	Rabbit	Goat Anti-Rabbit	Phoenix
PROKR1	1:250	Rabbit	Goat Anti-Rabbit	Caltag
PROKR1	1:100	Rabbit	Polymer	Sigma
PROK2	1:50	Goat	Rabbit Anti-Goat	Santa Cruz
PROKR2	1:50	Rabbit	Goat Anti-Rabbit	MBL
PROKR2	1:250	Rabbit	Goat Anti-Rabbit	Lifespan
PTGES	1:50	Rabbit	Goat Anti-Rabbit	Cayman
TRA-98	1:25	Rat	Goat Anti-Rat	Abcam

2.8.5 Secondary Antibody

After washing off the primary antibody in TBS twice for five min, biotinylated secondary antibody (diluted 1:500 in blocking serum) was applied to the tissue and incubated in a humidity chamber for 30 min. The secondary antibodies are raised against a species-specific sequence on the primary antibody. Therefore the type of secondary used depends on both the primary antibody and the NS used previously. Table 2.8 outlines which secondary was used with each antibody, and Table 2.9 describes the secondary antibodies.

For antibodies that were not readily detectable with standard secondary antibodies, a signal amplification polymer was used (Immpress reagent, Vector). This polymer was used undiluted on slides in place of a secondary antibody and streptavidin (see Tabel 2.10), followed by standard detection.

Table 2.10 Secondary Antibodies

Antibody	Manufacturer
Goat Anti-Rabbit	Vector
Goat Anti-Rat	Vector
Rabbit Anti-Goat	Dako
Rabbit Anti-Sheep	Vector

2.8.6 Visualization of Antibody

The secondary antibody was removed by rocking in TBS twice for five min. Streptavidin-horseradish peroxidase (HRP) (Vector) was diluted 1:1000 in TBS and applied to the slides for a 30 min incubation in the humidity chamber before being removed using TBS.

Some antibodies with low detectability levels were incubated with Streptavidin-ABC (Vector) in place of HRP (as outlined in each chapter). The complex was incubated for 30 min in an Eppendorf tube before usage as per manufacturer's instructions. The Streptavidin-ABC was dropped onto slides and incubated for 30 min as in the above protocol for HRP.

Antibody localisation was determined using 3,3-diaminobenzidine (liquid DAB+, DAKO). DAB chromagen was diluted in its buffer, according to the manufacturers' instructions. Sections were then incubated with DAB until staining was optimally detected (determined via use of light microscope). This process usually took ~60 sec, but possibly up to 5 min in some cases. The reaction was stopped by immersing the sections in water.

2.8.7 Counterstaining, Dehydration, and Slide Mounting

After antigen detection, the slides were counterstained using haematoxylin (no eosin) and mounted as described previously.

2.9 Fluorescent Immunohistochemistry

Fluorescent immunohistochemistry allows for more specific protein localisation within a tissue. It also allows antigens to be co-localised within the target tissue, so comparisons can be made. The general protocol for fluorescent immunohistochemistry is similar to that of DAB Immunohistochemistry (section 2.7) with some exceptions as described below.

2.9.1 Washes and Blocking Serum

All washes between treatments were performed in phosphate-buffered saline (PBS) instead of TBS for fluorescent immunohistochemistry. This also affects the blocking serum as it is changed to NS/PBS/BSA.

2.9.2 Primary Antibody

Concentration of primary antibody was adjusted as fluorescent detection is more sensitive. See the table for the dilutions used for fluorescent immunohistochemistry.

Table 2.11 Antibodies used for Fluorescent Immunohistochemistry

Primary Antibody	Dilution	Species Raised	Secondary	Manufacturer
3 β -HSD	1:5000	Rabbit	Goat Anti-Rabbit	Gift from Prof. Ian Mason
EP2	1:4000	Rabbit	Goat Anti-Rabbit	Cayman
EP4	1:2000	Rabbit	Goat Anti-Rabbit	Cayman
OCT4	1:150	Goat	Rabbit Anti-Goat	Santa Cruz
PROKR1	1:2000	Rabbit	Polymer	Sigma
PROKR2	1:500	Rabbit	Goat Anti-Rabbit	Lifespan
SMA	1:500	Mouse	Goat Anti-Mouse	Sigma
VASA	1:300	Rabbit	Goat Anti-Rabbit	Abcam

2.9.3 Secondary Antibody

The secondary antibodies used for fluorescence were peroxidase-conjugated (Table 2.12) rather than biotinylated as they were retrieved in a slightly different way.

Peroxidase antibodies were used at 1:500 and were diluted in NS/PBS/BSA.

Table 2.12 Secondary Antibodies

Antibody	Manufacturer
Goat Anti-Rabbit	Vector
Goat Anti-Mouse	Vector

2.9.4 Visualisation of Antibody

Rather than using Streptavidin detection, fluorescent immunohistochemistry utilises tyramide detection (TSA-Plus cyanine 3 system, Perkin Elmer). After the peroxidase secondary was washed off, a tyramide enhancement was applied diluted 1:50 in its own buffer as described by the manufacturer. The slides were then incubated in a dark humidity chamber for 10 min. The tyramide was removed with PBS in an opaque container to prevent any bleaching of the fluorescence.

2.9.5 Counterstain

The counterstain used for fluorescence varied depending on the colour of detection used for the primary antibodies (Table 2.13). They were diluted 1:1000 in PBS and applied to the slides for a 10 min incubation in a dark humidity chamber.

Table 2.13 Secondary Antibodies

Counterstain	Manufacturer
Propidium Iodide (Red)	Sigma
Sytox Green (Green)	Invitrogen
Dapi (Turquoise)	Sigma

2.9.6 Dehydration and Mounting

Fluorescent immunohistochemical slides do not need to be dehydrated. Instead they are mounted using Permaflur (Lab Vision Corp), a mounting medium for fluorescence. The slides are then stored at 4°C in the dark.

2.10 Co-localisation by Fluorescent Immunohistochemistry

In order to visualise two antigens in the same tissue the previous protocol (section 2.8) was followed by additional citrate retrieval in a microwave oven for 2 min boiling followed by the slides resting in the warm buffer for 20 min. Following the citrate retrieval, the above section (2.8) was repeated starting from the streptavidin/biotin blocking stage. Slides were kept in the dark as much as possible to preserve fluorescence, and the strongest primary antibody (one used at the highest dilution) was used first.

2.11 Microscopy

2.11.1 Light microscopy

Cellular sites of expression of target proteins were determined and slides photographed using a Provis AX70 (Olympus) microscope fitted with a camera (AxioCam HRc, Zeiss). Scale bars were generated using measurement slides and Adobe Photoshop CS5. This program was also used to compile photographic figures seen in the text.

2.11.2 Fluorescent microscopy

Slides were visualised using a Zeiss 510 META confocal microscope. Scale bars were embedded using the Zeiss software and images compiled into figures using Photoshop CS5.

2.11.3 Stereology / image analysis

Image analysis was performed on histological sections to quantify differences between treatment groups in various experiments. Several forms of image analysis were utilised as described below with the assistance of an Imager.A1 microscope (Zeiss) fitted with a Qicam Fast 1394 camera (Qimaging) and a ProScan II (Prior) image tiling device. Image-Pro Plus software (Media Cybernetics) was used to quantify images and calibrations were regularly checked.

Positive cells per area

For germ cell, apoptosis, and proliferative counts cells were stained for appropriate markers and the number of positive cells directly quantified. The area of the organ or tubule was determined. The positive cell count was then divided by the area to get an index of positive cells per area (Figure 2.1).

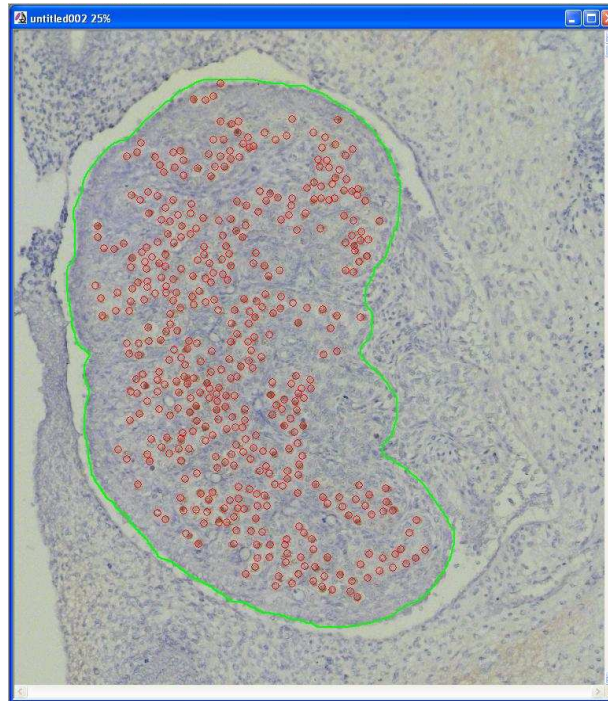


Figure 2.1 *Screen shot of germ cells per area count*

Fetal rat ovaries were analysed using Image-Pro Plus software, that allowed for positively stained cells to be quantified (red circles) and the area of the ovary to be measured (green outline) on the same piece of tissue.

Ovarian volume

Ovarian volumes were determined for e21.5 fetal rat ovaries by H&E staining every 10th slide of the serial sectioned ovary. A start and end point of the ovary was then determined and area taken from every slide containing ovarian tissue. These areas were then averaged and multiplied by the number of slides between the start and end of the ovary to determine volume.

Germ cell nuclear diameter

Quantification of nuclear diameter was performed as a measure of germ cell maturity. This measure was taken by tri-secting the nucleus of a cell and the subsequent measurement of each diameter. In order to get an accurate measurement of the variation of nuclear diameters in each specimen, multiple germ cells and slides were quantified as outlined in the following chapters.

2.12 Protein Extraction and Quantification

Proteins were extracted from primary tissue or cells with 50 µl RIPA buffer for primary tissue or 350 µl for cells (Section 2.13). Cellular samples were then snap frozen (-80 °C) for future use if not immediately needed. Before use, samples were homogenised with an electronic pestle (Sigma) with disposable tips (Sigma). This ensured maximum lysis of extracts.

2.12.1 Bradford Assay

Protein extracts were quantified by Bradford assay to determine concentration for further use. This was performed with the DC Protein Assay Kit (Bio-Rad) according to manufacturer's instructions, utilising a 96-well microplate (Corning). After 15 min incubation plates were scanned on a Multiskan EX microplate reader (Labsystems) at 590 nm. Specimens were then compared to a BSA standard curve run on the same microplate to determine protein concentration.

2.12.2 Western Blot

Protein samples were diluted in dH₂O to 30 mg in 13 µl. Thereafter, 5 µl of 4x SDS loading buffer and 2 µl of reducing agent (2-Mercaptoethanol, Sigma Aldrich) were added to each sample before denaturing at 85° C for 5 min on a Thermomixer (Eppendorf). Samples were cooled on ice and spun down (Eppendorf 5415D centrifuge) before loading into a 12% tris-HEPES-SDS Precise Protein gel (Thermo Scientific) alongside SeeBlue Plus2 protein standard (Invitrogen). Gels were run in a protein electrophoresis system (Bio-Rad) with running buffer (tris-HEPES SDS Buffer, Thermo Scientific) at 125v utilising a Powerpac (Bio-Rad) for 45-60 min or until the loading dye had run to the bottom of the gel.

Gels were then removed and washed in dH₂O for 10 min, then washed in transfer buffer (fast semi-dry buffer, Thermo Scientific) for 10 min. PVDF membrane (Millipore) was cut to the appropriate size for the gel and prepared for transfer by washing 1 min in methanol, 1 min in dH₂O, and 5 min in transfer buffer. Filter paper was prepared by soaking in transfer buffer. The gel and membrane were loaded with the filter paper into a semi-dry blotter as per manufacturer's instructions and run at 25v for 7-9 min depending on protein size.

The membrane was collected after transfer and washed in dH₂O, before being blocked in blocking buffer (1:1 PBS tween: Li-cor blocking buffer (Odyssey)). Primary antibodies were diluted in blocking buffer and the membrane was left to incubate at 4 °C overnight.

Membranes were washed in PBS tween the following morning for 15 min, then twice for 5 min, before being incubated with fluorescently labelled secondary antibodies diluted in blocking buffer for 1 hr at room temperature in the dark. Membranes were then washed x4 for 5 min in PBS tween, again in the dark, before detection on the Li-Cor Infrared Imaging System (Odyssey).

2.13 Cell / tissue culture

2.13.1 Stable transfection of PROKR1 T-Cam2 cells

In order to fully examine PROK1 signalling via PROKR1, the T-Cam2 germ cell line was stably transfected with the PROKR1 receptor. The creation of the PROKR1 construct was performed by Dr. Pamela Brown as follows:

The PROKR1 gene was subcloned from an Ishikawa vector (Evans *et al*, 2008) into a pLENTI6-derived destination vector containing a prolactin (PRL) peptide to ensure the receptor was expressed. A sequence for Blasticidin resistance was also part of the construct and used for later selection.

Cells were transfected alongside a similar construct containing GFP, as a positive control for transfection.

Linearisation

Both constructs (GFP and PROKR1) were linearised using the restriction enzyme NaeI (New England Bio) as per manufacturer's instructions before transfection, in order to increase the number of cells integrating the plasmid in their DNA. Cells were also transfected with the plasmid uncut (super-coiled), as this increased the number of plasmids to enter the cells initially. A 2 µl sample of the linearised plasmid and supercoiled plasmid were run on a gel to verify the linearised sample was fully cut before transfection.

Ethanol Precipitation and Quantification of DNA

Digested plasmid was then purified and concentrated using ethanol precipitation. This was performed by adding 100 µl dH₂O to the plasmid, followed by 20 µl Sodium Acetate (Sigma) (3M, pH 5.2) and 3 volumes of pure ethanol (660 µl). This was mixed and incubated at -20° C for 20 min to speed up precipitation of DNA. The sample was then centrifuged at full speed for 10 min at 4 °C and the supernatant carefully removed. Then 500 µl 70% ethanol was added to remove salt and further spun at 4 °C for 5 min. The supernatant was removed and the tube left open for the remaining ethanol to evaporate. The pellet was re-suspended in 20 µl TE and left at 4 °C overnight. Plasmids were quantified using a Nanodrop spectrophotometer (Thermo Scientific).

Transfection

Cells were plated in 150mm diameter cell culture plates (Corning) 2 days prior to transfection to ensure maximum transfection efficiency. 15 µg of DNA from each plasmid was incubated with 60 µl TransIT –LT1 transfection reagent (Mirus) for 20 min in an Eppendorf tube. The solution containing the plasmid was then dropped onto the plates with newly added media and mixed by gentle rocking.

The T-Cam2 cells were left overnight with the transfection solution in the media. The next morning medium was changed on the plates and a selection medium was applied, consisting of normal T-Cam2 medium with 10 µg/ml Blastacidin (Invivogen). This killed off any cells that had not been transfected, or in which the plasmid was not correctly integrated. This selection medium was used for 12 days

post transfection and the medium was changed every 2 days to ensure dead cells were removed promptly (prevented transfected cells from being adversely affected by dying cells).

PROKR1 T-Cam2 cells were then trypsinised as in normal passaging (section 2.10.11), and kept in a 25 cm² flasks. Standard maintenance medium as described in section 2.13 was then used (with only 2 µg/ml Blasticidin). At this stage linearised transfections were abandoned as transfection was low if at all successful. All experiments were done using the supercoiled plasmid for PROKR1. Cells were frozen periodically for stock in 1.5 ml Bambanke freezing medium (Lymphotec). Heightened expression of PROKR1 was confirmed via qRT-PCR and Western blot analysis.

2.13.2 Stable cell culture maintenance

T-Cam2 wild-type and PROKR1 transfected cells were kept in T-Cam2 medium as described below (Section 2.14) at 37 °C with 5% CO₂. The cells were maintained in 162cm² flasks and passaged every 3-4 days using 0.5% Trypsin/EDTA (Gibco). Trypsin was added for 5 min and cells were put back in the incubator to accelerate their detachment. Cells were then split 1:4 in the case of wild-type or 1:3 in the case of PROKR1 cells.

Ishikawa cells stably transfected with the PROKR1 gene (Evans *et al*, 2008) were used as a positive control. They were maintained in the media described in Section 2.14 in the same culture conditions as the T-Cam2 cells. They were split every 3-4 days at a ratio of 1:5.

2.13.3 Organ culture

For organ culture analysis of fetal gonads, tissue was micro-dissected as described above (Section 2.1). First trimester gonads were halved, with one piece of each gonad going into the treatment group and the other into control (Table 2.13). Second trimester gonads were dissected into small pieces which were randomised and put into treatment groups. Small pieces of tissue were taken from each specimen as a 'time 0' control to determine tissue quality before being put into culture.

Droplets of 30 μ l of organ culture media (as described in section 2.14) were placed on the lid of a 10cm² square dish (Corning). Each piece of gonad was delicately placed into the droplets using needles. The bottom of the dishes was filled with 10ml dPBS (Gibco) to keep tissue hydrated. The lid was then quickly turned and placed on top of the bottom of the dish, suspending the organ pieces in the media. This technique was devised to mimic *in vivo* surface tension and prevent necrotic effects of direct exposure to culture plates and/or filters, and has been utilised successfully for fetal gonad culture in several organisms, thus potentially proving a better model for human fetal culture possibly resulting in better tissue quality post-culture (Zhang *et al*, 2008; Szczepny *et al*, 2009).

Tissue was removed from the media droplets after the appropriate amount of time (Table 2.14) and snap frozen (-80 °C) or fixed for further analysis.

Table 2.14 Organ culture treatments

Treatment	Manufacturer	Amount	Tissue/Purpose	Culture Time
PGE ₂	Sigma	100nM	Ovary/Histology	8 or 24 hours (as specified)
PROK1	Peprtech	40nM	Ovary and Testis/Culture	24 hours

2.13.4 Testicular interstitial cell culture

Fetal testes were removed from early second trimester fetal specimens and extraneous material removed via micro-dissection. The testes were then transferred into a glass dimple slide containing 100 μ l Collagenase IV (Sigma) (1mg/ml in HBSS (Sigma)) and teased apart using needles until pieces were small enough to pipette. Tissue was then transferred into a 1.5 ml tube (Eppendorf) and the slide washed 4 times with 100 μ l Collagenase each time adding wash to the tube (making the total volume 500 μ l).

The sample was incubated at 37 °C for 5 min, mixing at 650 rpm (Thermomixer, Eppendorf). The sample was mixed via pipetting to ensure a one-cell suspension and incubated for a further 5 min. DNase I (Sigma) (10 μ l of 10mg/ml in HBSS) was added to the suspension to reduce viscosity and samples were then incubated for a further 5 min with this addition.

To remove the Collagenase, the cells were centrifuged at 800g for 5 min. The supernatant was discarded and the sample re-suspended in 1 ml HBSS. This wash process was repeated for a second time, and a small portion of cells removed for a 'time 0' control. Cells were then washed in testis culture medium (Section 2.13) spun down a final time, and re-suspended in 1 ml medium. Cells were run through a 70 μ m cell strainer to ensure a single-cell suspension, and plated into 2 wells of a 6-well plate (500 μ l each well) that had been coated with 0.1% sterile gelatine (Sigma).

Cells were allowed to adhere to the plate surface overnight. Medium was changed in the morning, with one well getting 40 nM PROK treatment and the other receiving the dH₂O vector control. Cells were left to incubate for 24 hours, and then lysed in RLT buffer for mRNA analysis.

2.14 Commonly Used Solutions

Acid Alcohol

Acid alcohol is prepared using 70% ethanol with 1% concentrated HCl.

Blocking Serum

Normal serum (Biosera) was diluted 1:4 in TBS or PBS as appropriate with 5% bovine serum albumen (BSA) (Sigma).

Citrate Buffer

42.02g Citric acid monohydrate was diluted in 900 ml distilled water, and brought to pH 6.0 using NaOH.

Freezing Medium

Storage of cell lines was performed by freezing cells down in Bambanker freezing media (Lymphotec).

Ishikawa Medium

PROKR1 transfected Ishikawa cells were cultured in Dulbecco's Modified Eagles Medium (DMEM) with Glutamax (Gibco), supplemented with 10% heat inactivated fetal bovine serum (FBS) (Gibco), 200 μ g/ml G418 (Invivogen).

Ishikawa Starving Medium

PROKR1 transfected Ishikawa cells were starved in DMEM Glutamax, with no supplementation.

Peroxide Blocking Solution

3% by volume hydrogen peroxide (Fisher Scientific) (30mls of 30%) added to methanol (270 mls) (Fisher Scientific).

NP40 / RIPA Lysis Buffer

Lysis buffer was prepared with 150 mM NaCl (Sigma), 50 mM Tris.HCl, pH7.5 (Sigma), 1% NP40 and 0.25% sodium deoxycholate brought to pH 7.4 with HCl. A protein inhibitor mini tablet (Roche) and 20 µl sodium vanadate (New England Biolabs) per 10 ml of solution was added immediately before use.

Organ Culture Media

Fetal testis and ovary samples were cultured whole or in pieces (1mm²) in α MEM (Gibco), supplemented with 3% BSA, 1% 100x Non-Essential Amino Acids (NEAA) (Gibco), 1% 200mM L-glutamine, 1% Penicillian-streptomycin (Lonza), 1% Sodium pyruvate (Gibco), and 0.002% ITS (Lonza). Media was filter sterilised before use.

Phosphate-Buffered Saline (PBS)

PBS used for fluorescent immunohistochemistry and western blotting was prepared by adding 1 PBS tablet (Sigma) consisting of 0.01M phosphate buffer, 0.0027 M potassium chloride, and 0.137 M NaCl with a pH of 7.4 to 200 ml distilled water.

Scott's tap water

Scott's tap water was prepared by adding 10 g Potassium hydrogen carbonate and 100 g Magnesium sulphate to 5000 ml tap water.

T-Cam2 Medium

T-Cam2 cells were cultured in RPMI medium, supplemented with 10% heat inactivated FBS and 1% 100x L-glutamine. Blasticidin (2 µg/ml) was added to PROKR1 transfected T-Cams only.

T-Cam2 Starving Medium

T-Cam2 cells were starved in RPMI medium, supplemented with 2mM L-glutamine.

Testicular Interstitial Culture Medium

Interstitial cell cultures derived from fetal testis tissue, were maintained in phenol-red free DMEM, supplemented with 10% FBS, 1x NEAA2mM L-glutamine, 1% Penicillian-streptomycin, 1% amphotericin (Sigma), and 1% D-(+)-Glucose (45% solution; Sigma). In addition, 10 IU of hCG was added to each ml of medium to ensure normal steroidogenesis was promoted. Medium was filter-sterilised before use.

Tris-Buffered Saline (TBS)

TBS used for DAB immunohistochemistry was prepared by adding 121.1g Tris base (Sigma) and 170g NaCl to 2000 ml distilled water, and brought to pH 7.4 with HCl.

Chapter 3

Prostaglandin E₂ in fetal ovarian development

Chapter 3. Prostaglandin E₂ in fetal ovarian development

3.1 Introduction

PGE₂ is a potent mediator of cellular migration, proliferation, and vascularisation (Diazflores *et al*, 1994; Wang & DuBois, 2006). Within female reproduction, PGE₂ plays well-recognised and important roles in tissues such as the ovary, endometrium, myometrium, and cervix (Oates *et al*, 1988b; Oates *et al*, 1988a; Sales & Jabbour, 2003a). PGE₂ is a well-characterised regulator of ovulation and fertilisation but its role in early ovarian development or function has not been investigated. Despite this lack of information, it is known that PGE₂ and other prostaglandins such as PGD₂ can induce expression of the neurotrophins, known regulators of early ovarian development (Anderson *et al*, 2002b; Spears *et al*, 2003; Kerr *et al*, 2009; Childs *et al*, 2010a), in astrocyte cultures (Toyomoto *et al*, 2004). In addition to Toyomoto's work, recent studies conducted by colleagues at the University of Edinburgh have also identified PGE₂ as a mediator of the neurotrophins in the human female reproductive tract (Jabbour, unpublished). This link suggests PGE₂ may play an up-stream role in the pathway controlling human ovarian development and possibly primordial follicle formation.

PGE₂ is derived step-wise from arachadonic acid by the cyclooxygenase enzymes (COX1 and 2), and the PGE₂ specific synthase, PTGES (Figure 3.1) (Funk, 2001). COX1 and 2 play differing roles in the production of downstream prostanoids, as COX1 is constitutively expressed in many cell types, whereas COX2 is an inducible enzyme synthesised in response to cytokine action (Sales & Jabbour, 2003b). PTGES, unlike the COX enzymes, is a specific terminal prostanoid synthesis enzyme which controls conversion of PGH₂, a prostanoid intermediate, to PGE₂ (Forsberg *et al*, 2000). After synthesis, PGE₂ signals through one of four GPCRs (EP1-4) to elicit its targeted response (Narumiya *et al*, 1999). The EP receptors are able to regulate differing downstream intracellular cascades (Section 1.10; (Alfranca *et al*, 2006)), allowing PGE₂ to mediate various functions in the same tissue (Coleman *et al*, 1994). Additionally, as PGE₂ is a lipid mediator with a short half-life, causing its action to be restricted to cells close to sites of PG secretion, this allows for paracrine or autocrine regulation, and thus cell specific control, as compared to hormones which can act systemically (Negishi *et al*, 1995).

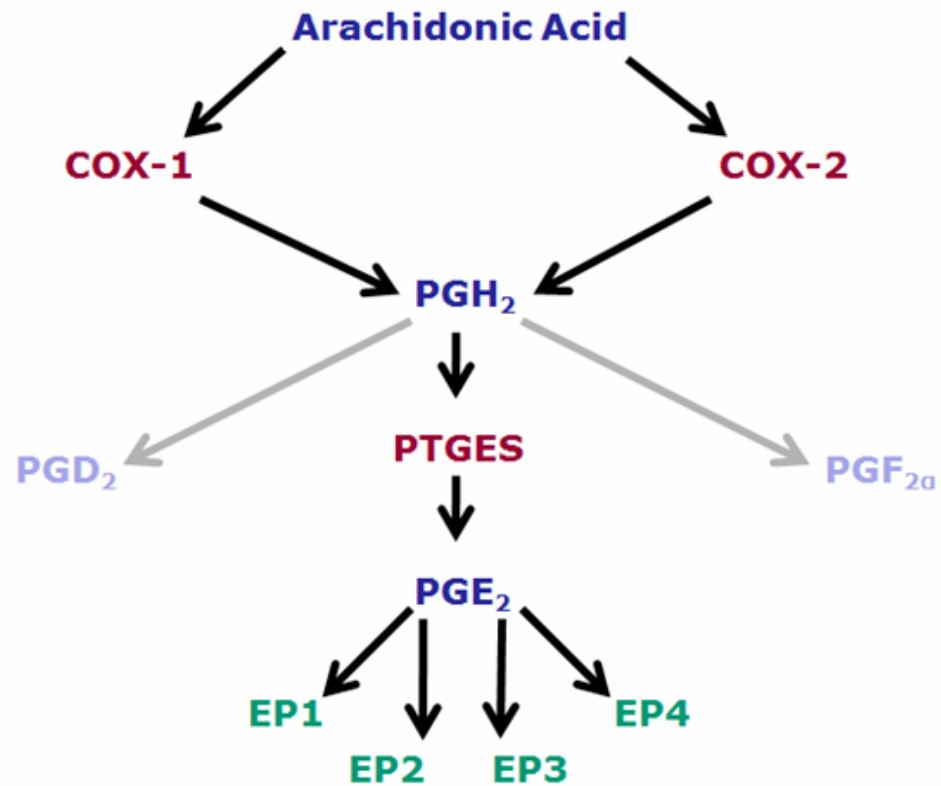


Figure 3.1 Prostaglandin E₂ synthesis and signalling pathway.

PGE₂ is synthesised from arachidonic acid by the action of the cyclo-oxygenase enzymes (COX1 or 2) to produce the intermediate PGH₂. This intermediate is further converted by specific terminal enzymes such as PTGES (in the case of PGE₂) to form prostanoids including PGD₂, PGE₂ and PGF_{2α}. After synthesis PGE₂ is able to signal via four G-coupled protein receptors (EP1-4). Synthesis enzymes are noted in red, lipids in blue and receptors in green.

In order to fully explore what role PGE₂ might play in early ovarian development, the expression of its precursor enzymes (COX1, COX2, and PTGES) as well as its receptors (EP1-4) were characterised. These enzyme and receptor targets were examined across the first and second trimester, with both transcript levels and protein localisation identified. Receptors which were deemed to have discrete germ cell localisation were further inspected to determine if their expression was limited to a specific subset of oogonia. In addition, human fetal ovarian tissue was cultured with PGE₂ and analysed for alteration in expression of germ cell markers and known regulatory factors. Subsequent cultures were performed to identify histological changes to further identify a function for PGE₂ in the developing ovary.

3.2 Materials and Methods

Tissue collection

Human fetal tissue used in the following experiments was obtained and dissected as described previously (Section 2.1), with subsequent SRY genotyping to determine sex of first trimester specimens (Section 2.3).

RNA extraction and cDNA synthesis

Sample tissue was then processed to extract RNA and subsequently cDNA synthesised for genomic analysis as previously discussed (Section 2.4).

Quantitative RT-PCR

In order to determine if mRNA transcripts encoding PGE₂ precursor enzymes (COX1, COX2, and PTGES) and receptors (EP1-4) varied across gestation, qRT-PCR was performed using the ABI 7500Fast system and either SYBR Green or Taqman analysis as described in Section 2.5.

Quantitative RT-PCR analysis of human fetal cultures was also performed using the ABI 7900HTFast system and SYBR Green analysis to determine any changes in germ cell marker expression (OCT4, VASA, DAZL) and known ovarian regulators (BDNF, NTF5, MCL-1, INHBA, SMAD2, SMAD3); details of this protocol are also outlined in Section 2.5.

Immunohistochemistry

Human fetal ovarian samples were used to localise PGE₂ precursor enzymes (COX1, COX2, and PTGES) and receptors (EP1-EP4) to determine cell-specific sites of PGE₂ synthesis and action. Varying germ cell maturity markers were also utilised to determine if specific receptors were developmentally related (VASA, OCT-4). Finally, immunohistochemistry was also utilised to determine changes in apoptosis (CC3) and proliferation (BrdU). Protocols for these localisations can be found in Section 2.8.

Human fetal ovarian culture

Second trimester fetal ovaries (n= 6, 15-17 weeks gestation) were cultured as small explants on culture inserts as described previously (Martins da Silva *et al*, 2004). Tissue was cultured using organ culture media as described in Section 2.13. Tissue was split into 3 treatment groups: no treatment, 3 µg/ml indomethacin (Sigma) with vehicle (ethanol), or 3 µg/ml indomethacin with 100nM PGE₂. Indomethacin was utilised to reduce endogenous PG production which may have masked effects of the exogenous PGE₂ treatment. Tissue cultured for transcript expression analysis was cultured for 8 hours, subsequently snap-frozen (-80 °C) followed by RNA extraction as described in Section 2.4. These cultures were performed by Dr. Rosey Bayne.

A second series of experiments were performed for histological analysis (n=5, 15-17 weeks gestation). Tissue was cultured in hanging drops with treatment as above for 24 hours with BrdU and subsequently fixed in Bouins solution and processed as in Section 2.5.

Stereology/Image Analysis

Histological changes after PGE₂ treatment in the human fetal ovary were determined via image analysis using various markers as described in section 2.10.9.

Measurements of proliferation were performed using 5 slides from each sample at least 10 sections apart (50 microns). Positive cells (BrdU) were counted and ovarian area taken (necrotic tissue as the result of the culturing process was not taken in to account in this analysis, and the amount of necrotic tissue was not seen to vary between treatment groups). This method was deemed to be more than necessary for accurate quantification, with subsequent apoptotic counts (CC3) performed on 3 slides from each sample rather than 5 slides.

Statistical Analysis

Quantitative RT-PCR data were analysed with GraphPad Prism version 4 statistical software (GraphPad Software Inc). Gestational comparison data were analysed using one-way ANOVA, data were then either analysed as described or log-transformed for further analysis. Log-transformation was performed in instances where data sets did not fit a Gaussian distribution. The Kolmogorov-Smirnov normality test was used for this purpose.

Data were then analysed utilising the Newman-Keuls Multiple Comparison post-test to determine significant changes between gestational values. This post-test was chosen as has more strength than a Tukey post-test and the risk of type I error does not occur with only three groups (as in our study). Some data was also analysed using a post-test for linear trend, this test was performed when data were in a natural order (ie across gestation).

Gene expression changes identified using qRT-PCR after PGE₂ treatment of human fetal ovaries were also analysed using GraphPad Prism as above. Data were analysed using paired t-tests on log-transformed data comparing PGE₂ treated tissue to indomethacin-only treated tissue (as the appropriate control).

Stereology/image analysis data were analysed using the above statistical software, with Student's t-test to determine difference between treatment groups.

3.3 Results

3.3.1 Precursor enzymes of PGE₂ are up-regulated at initiation of primordial follicle formation

To determine the presence and pattern of expression of mRNA transcripts encoding PGE₂ precursor enzymes during human fetal ovarian development, qRT-PCR was performed for *COX1*, *COX2* and *PTGES* across a range of gestations. Ovarian specimens were grouped into three gestational stages to broadly reflect the key developmental events of early to mid-gestation ovarian development, namely the proliferation of undifferentiated PGCs (8-11 weeks gestation), the formation of germ cell nests and entry of the first germ cells into meiosis (13-16 weeks), and on-going meiotic entry and the onset of primordial follicle formation (17-20 weeks).

Transcripts encoding all precursor enzymes were detected in the human fetal ovary, as shown in Figure 3.2. Expression of transcripts encoding *COX2* increased across gestation, being expressed at low levels at 8-11 weeks gestation ($0.5 \pm 0.2 \times 10^{-7}$, relative to the housekeeping gene *GAPDH*), increasing at 13-16 weeks gestation ($3.9 \pm 1.0 \times 10^{-7}$ relative to *GAPDH*) and again at 17-20 weeks gestation ($5.4 \pm 2.2 \times 10^{-7}$ relative to *GAPDH*, linear trend $p=0.02$, $n=5-7$ per group, Figure 3.2B).

Additionally, the PGE₂ specific enzyme *PTGES* was significantly decreased at early second trimester compared with both first and late second trimester (2.3 ± 0.2 and 1.8 ± 0.2 compared to $0.8 \pm 0.1 \times 10^{-1}$ relative to *GAPDH*, $p=0.002$ and 0.008 respectively, Figure 3.2C). However, no change was seen in the transcripts encoding the constitutively expressed precursor enzyme *COX1* ($p=0.79$, Figure 3.2A). These data reveal transcripts encoding the PGE₂ precursor enzymes *COX2* and *PTGES* are up-regulated in late second trimester coincident with initiation of primordial follicle formation. In addition, *PTGES*, which specifically synthesises PGE₂, displays a bi-phasic pattern as it is heightened in first trimester as well as late second trimester.

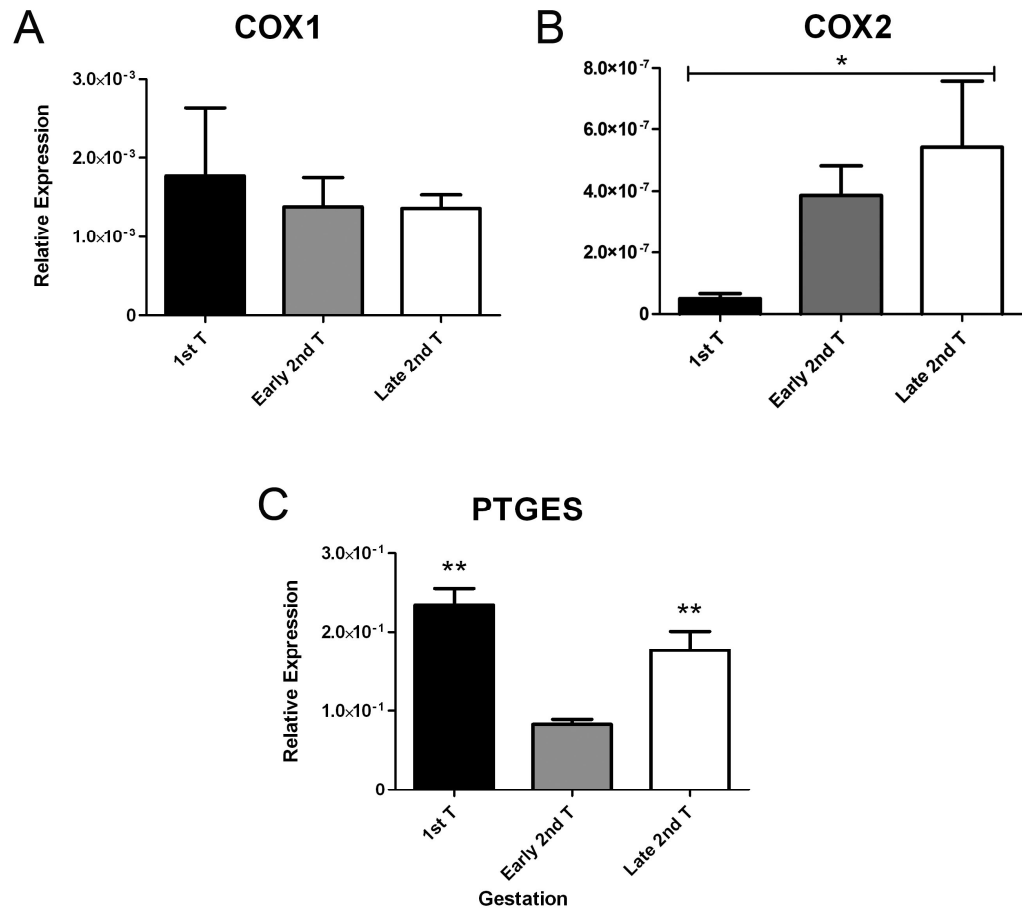


Figure 3.2 *Genes encoding the PGE₂ precursor enzymes are up-regulated at initiation of primordial follicle formation.*

Expression of the three enzymes necessary to synthesise PGE₂, was analysed by qRT-PCR across gestation and split into age groups concordant with gestational events; PGC proliferation in 8-11 weeks (1st T), meiosis and germ cell nest formation in 13-16 weeks (Early 2nd T), and primordial follicle formation in 17-20 weeks (Late 2nd T; n= 5-7 samples for each gestation). (A) Expression of COX1 did not change during early ovarian development. (B) COX2 expression was significantly up-regulated at late 2nd trimester (*=p<0.05 determined by test for linear trend). (C) Transcript levels for PTGES were significantly increased at both 1st and late 2nd trimester, compared with expression at early 2nd trimester gestation (**=p<0.01). All data are expressed as a relative expression, normalised to the housekeeping gene *GAPDH*.

3.3.2 EPs required for PGE₂ signalling are expressed and developmentally regulated in the fetal ovary

Further examination was performed to determine the expression of transcripts encoding the four GPCRs necessary for PGE₂ signalling using the gestational range outlined above. EP1, 2, and 4 displayed similar expression patterns (Figure 3.3 A, C, D), increasing transcript expression with increasing gestational age. However, only EP4 showed a significant change across gestation. Expression of EP4 was low at 8-11 weeks gestation ($0.5 \pm 0.3 \times 10^{-3}$ relative to *GAPDH*), increased at 13-16 weeks ($1.1 \pm 0.3 \times 10^{-3}$ relative to *GAPDH*) and again at 17-20 weeks gestation ($1.6 \pm 0.3 \times 10^{-3}$ relative to *GAPDH*, linear trend $p = 0.3$, Figure 3.3D). EP1 and EP2 displayed a similar trend, however this did not reach significance ($p = 0.16$ and 0.35 respectively). EP3 did not show a similar trend to the other receptors, displaying high variability in early 2nd trimester, with no significant changes in transcript expression across gestation ($p = 0.49$, Figure 3.3B). Outwith expression pattern, it is also notable that EP3 and EP4 are expressed at higher levels than that of EP1 and EP2. These data suggest EP3 and EP4 may play a more predominant role during human fetal ovarian development, and that the role of EP4 increases with development leading to primordial follicle formation.

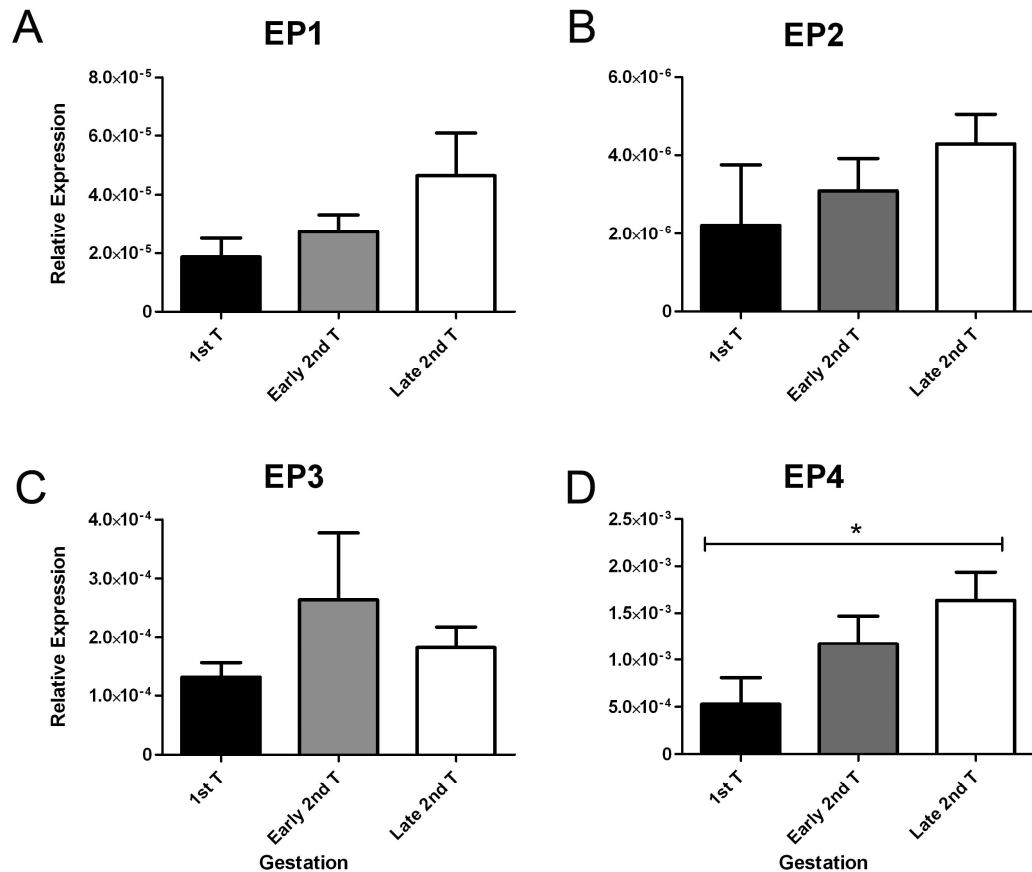


Figure 3.3 PGE₂ receptor mRNA expression across gestation

Expression of the four receptors (EP1-4) necessary for PGE₂ signalling, was analysed by qRT-PCR across gestation and split into age groups concordant with gestational events; PGC proliferation in 8-11 weeks (1st T), meiosis and germ cell nest formation in 13-16 weeks (Early 2nd T), and primordial follicle formation in 17-20 weeks (Late 2nd T; n= 4-6 samples for each gestation). Expression of (A) EP1 (B) EP2 and (C) EP3 did not change during early ovarian development. (D) Transcript levels for EP4 are significantly up-regulated across gestation (*= $p < 0.05$, determined by test for linear trend). All data are expressed as a relative expression, normalised to the housekeeping gene *GAPDH*.

3.3.3 Developmentally-regulated precursor enzymes are germ cell specific

To determine the site of PGE₂ production, immunohistochemistry was performed using human fetal ovarian tissue to detect the precursor enzymes required for PGE₂ synthesis. COX1 protein was localised to the pre-granulosa cells closely associated with germ cells within the germ cell nests. No expression was seen in the germ cells or the interstitial cells within stromal cell streams (Figure 3.4A-B). Conversely, COX2 was not seen in pre-granulosa cells or stromal cell streams; rather being expressed in a germ cell-specific manner with varying intensity of expression seen in specific germ cells and distinct staining of primordial follicles (Figure 3.4C-D). PTGES, the PGE₂ specific enzyme, was also germ cell-specific with consistent expression throughout the germ cells (Figure 3.4E-F). The expression patterns noted for the PGE₂ precursor enzymes determines that PGs in the ovary can be derived from the breakdown of arachadonic acid by COX1 in the pre-granulosa cells or by COX2 in the germ cells, but that final conversion into functional PGE₂ occurs exclusively in the germ cells within the human fetal ovary.

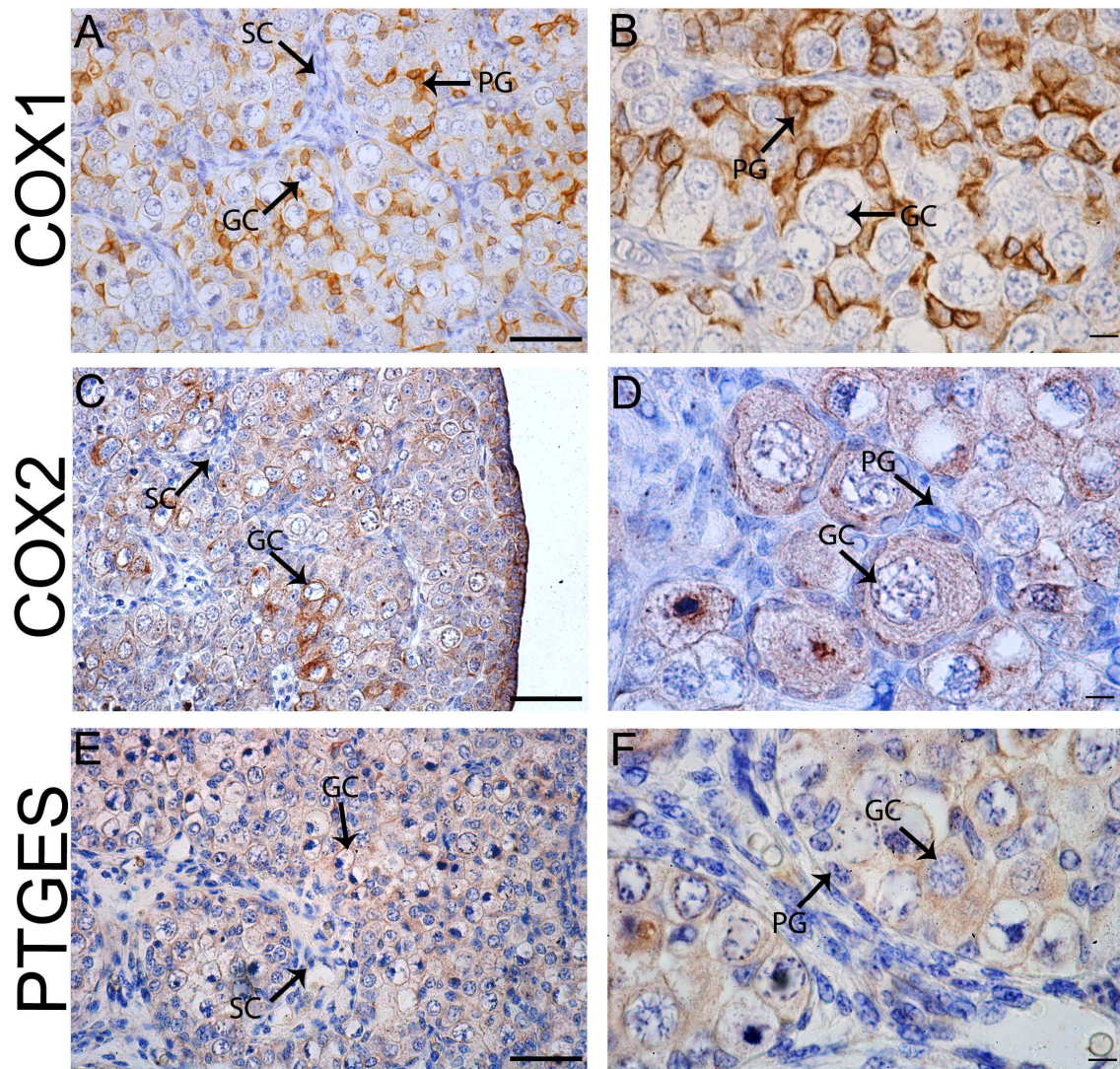


Figure 3.4 *Immunohistochemical detection of the PGE₂ precursor enzymes in the human fetal ovary.*

Prostaglandin synthesis enzymes were localised in second trimester human fetal ovarian tissue using 3,3'-diaminobenzidine tetrahydrochloride staining (brown). (A-B) COX1 is pre-granulosa cell specific, staining somatic cells within the germ cell nests. (C-D) COX2 is germ cell specific, with no staining detected in stromal cell streams or pre-granulosa cells. Additionally, intensity of COX2 staining varied between neighbouring germ cells. (E-F) PTGES was also localised to germ cell nests but expression was consistent across germ cells. Scale bars equal 50 microns (A, C, and E) and 10 microns (B, D, and F). Images are a composite of several stained tissues, with each antibody utilised on at least three separate tissues from specimens of varied ages to confirm localisation and identified any differences in expression across gestation.

3.3.4 PGE₂ receptor expression is primarily localised to the germ cells in the human fetal ovary

In order to determine the cell-specific sites of PGE₂ action in the human fetal ovary, immunolocalisation was performed to detect each of the four EP receptors. EP2 and EP4 displayed similar sites of expression, with the germ cells appearing to be the sole location for both receptors (Figure 3.5C, D, G, and H). However, EP2 and EP4 localisation was discrete, with EP2 staining only expressed in the more central germ cells (ie the most mature) with distinct staining of primordial follicles, whereas EP4 staining was primarily localised to the immature germ cell population near the periphery of the ovary. EP3 displayed expression in both pre-granulosa cells and germ cells within germ cell nests, as well as strong expression in the epithelial layer of the ovary (Figure 3.5 E-F). EP1 expression was notably weaker than that of the other EP receptors, with expression in cells lining blood vessels and the blood cells within, but no notable expression in surrounding ovarian tissue (Figure 3.5A-B). These data demonstrate that three of the EP receptors are capable of directly regulating the germ cells, and germ cells appear to be the sole site of expression of EP2 and EP4. Additionally, these data also highlight the possibility that EP2 and EP4 may play a role in distinct subsets of germ cells.

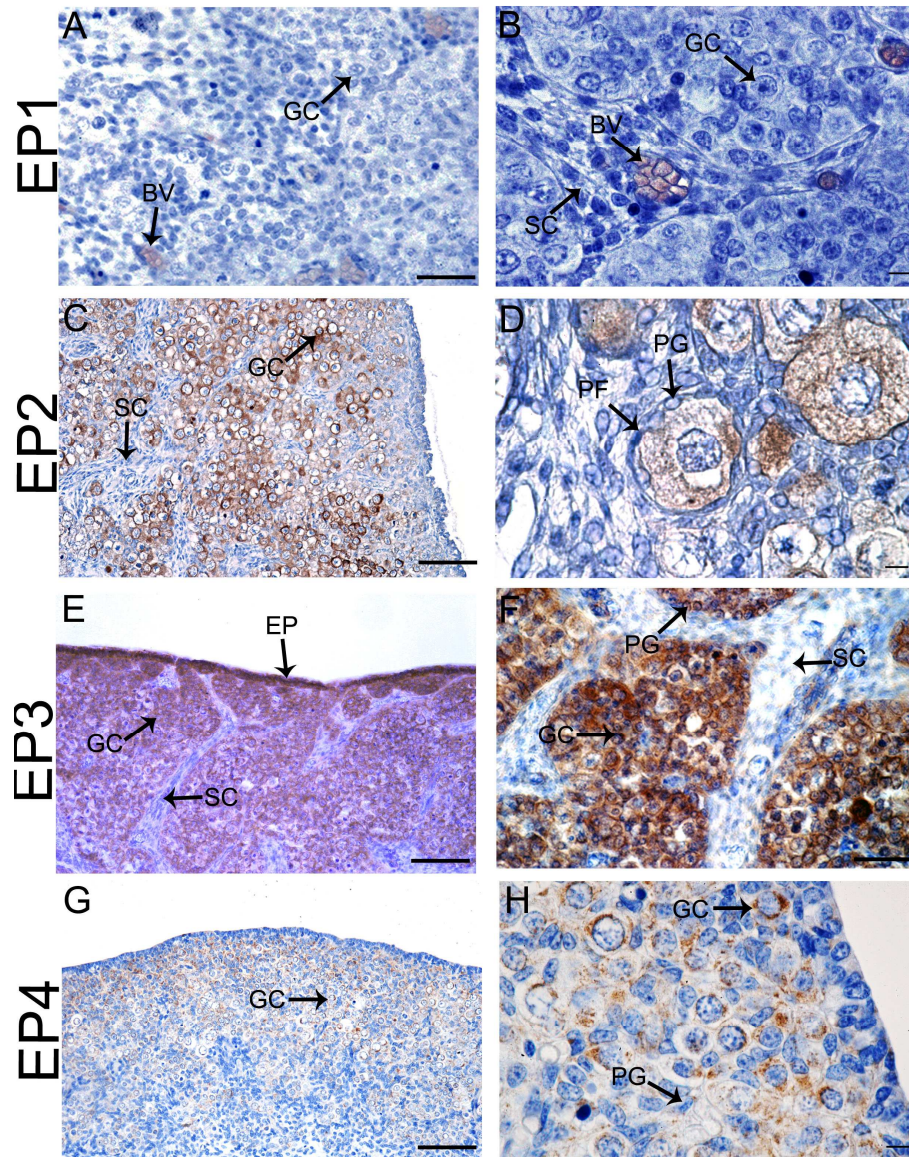


Figure 3.5 *Immunohistochemical detection of the PGE₂ receptors in the human fetal ovary.*

The PGE₂ receptors EP1-4 were localised in second trimester ovarian tissue using 3,3'-diaminobenzidine tetrahydrochloride staining (brown). (A-B) EP1 was limited to the blood vessels (BV) with no staining of germ cells (GC). (C-D) EP2 was localised to a discrete population of GC and primordial follicles (PF) with no staining seen near the periphery of the ovary, in somatic cells (SC) or pre-granulosa (PG) populations. (E-F) EP3 was the most ubiquitously expressed PGE₂ receptor with clear staining throughout the GCs and PGs, with additional staining in the epithelial layer (EP). (G-H) EP4 was localised to the GCs, and appeared to display more expression near the periphery of the ovary and less in the medulla. Scale bars equal 100 microns (E, G, and C), 50 microns (A and F) and 10 microns (B, D, and H). Images are a composite of at least three separate tissues from specimens of varied ages.

3.3.5 EP2 and EP4 rarely co-localise in the human fetal ovary

To further determine site-specific roles of EP2 and EP4, co-localisation was performed in second trimester ovarian tissue. Both EP2 and EP4 were expressed as previously demonstrated in Figure 3.5; EP2 was expressed discreetly in the centre of the ovary, whereas EP4 expression was more widespread but concentrated at the periphery (Figure 3.6). Low magnification images suggest little co-localisation of the two receptors (Figure 3.6A); however, higher magnification shows that the receptors are expressed in the same cells near the middle of the ovary (Figure 3.6B). Expression of the receptors on co-localised cells was often not interspersed, rather one side of the cell expressed EP2 and the other EP4. These images demonstrate that although EP2 and EP4 receptors are primarily expressed in differing germ cell populations, their sites of action are not mutually-exclusive. Additionally, they often display a expression on opposite sides of a germ cell when co-localised.

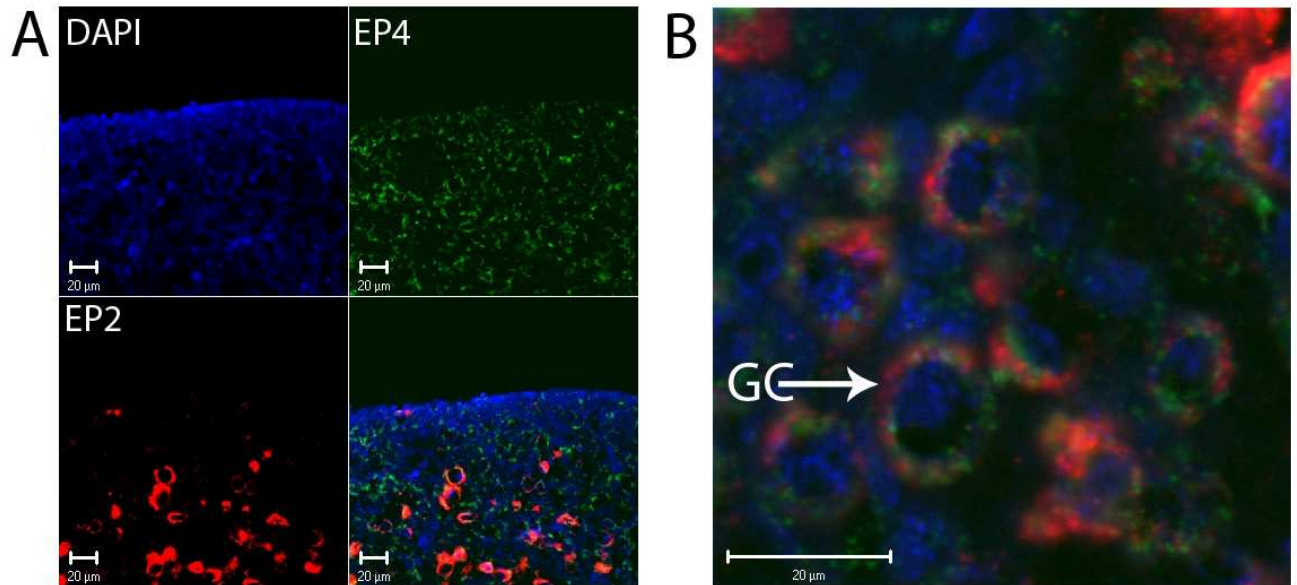


Figure 3.6 *Co-localisation of EP2 and EP4 in the human fetal ovary.*

The germ cell-specific receptors EP2 and EP4 were examined in 17 week gestation human fetal ovarian tissue. (A) EP2 (red) and EP4 (green) were expressed in the germ cells (GC) of the human fetal ovary with rare co-localisation (yellow). (B) Cells in which both receptors were co-expressed showed polar localisation of the two receptors with EP2 on one side and EP4 on the other (arrow). Dapi counterstain (blue) was utilised and scale bars equal 20 microns. Images are representative of staining performed on three separate second trimester tissues.

3.3.6 EP2 expression is limited to more mature oogonia and oocytes within primordial follicles

As EP2 expression appeared to be restricted to maturing germ cells, co-localisation with the immature germ cell (PGC) marker OCT4 was performed, alongside co-localisation with a mature germ cell marker VASA (Anderson, 2007). No co-localisation of EP2 and OCT4 was determined in the human fetal ovary (Figure 3.7). OCT4 was seen to stain the immature PGCs on the periphery of the ovary, whereas EP2 was localised to the centre of the ovary (Figure 3.7A). There was some interspersed OCT4 positive cells nearer to the centre of the ovary but none of these cells expressed EP2 (Figure 3.7B).

VASA expression was shown in most germ cells in the human fetal ovary, bar the PGC layer near the epithelium of the ovary (Figure 3.8A). EP2 was also lacking in these PGCs, but EP2 expression was restricted to an even more mature population than that of VASA, with a distinct band of VASA positive germ cells nearer the periphery that were EP2 negative. In addition, in the centre of the ovary, primordial follicles could be identified which contained oocytes positive for both VASA and EP2. These data demonstrate the PGE₂ receptor EP2 is exclusively located on the more mature germ cells in the human fetal ovary, including oocytes within primordial follicles.

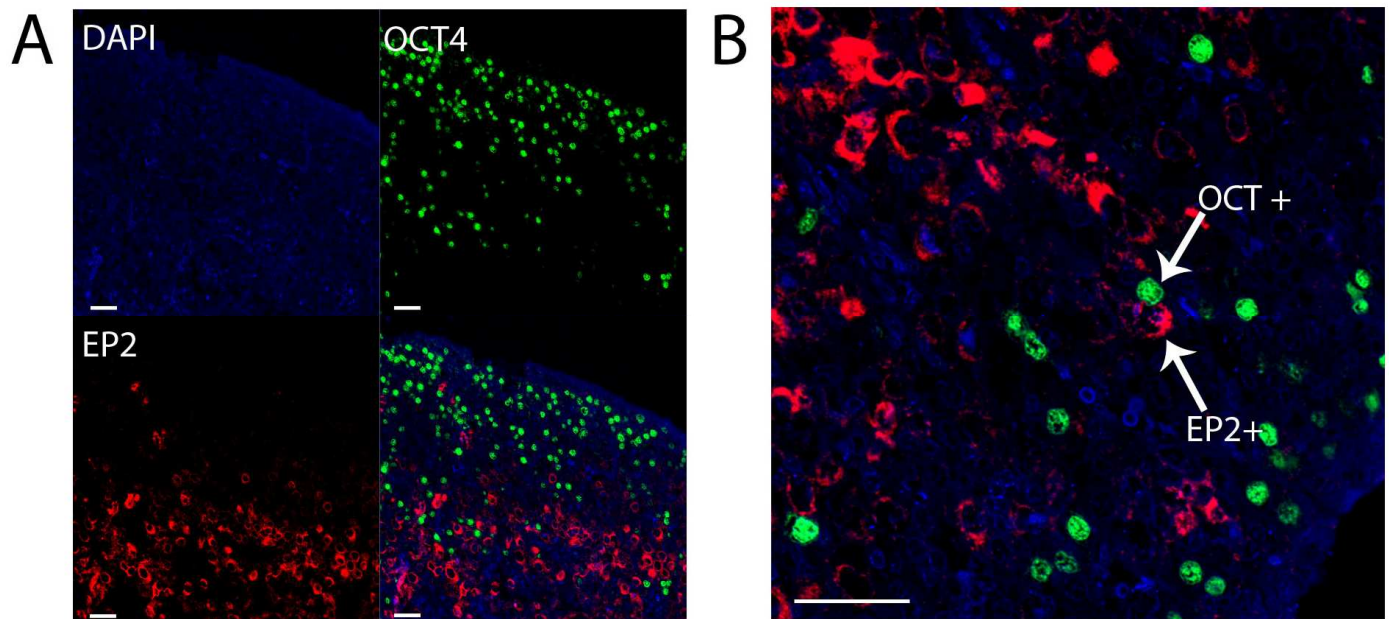


Figure 3.7 *EP2 is not expressed by PGCs in the human fetal ovary*

EP2 (red) and the immature germ cell marker OCT4 (green) were dual expressed in 19 week human fetal ovarian tissue. (A) OCT4 was restricted to a band of PGCs near the epithelium of the ovary, whereas EP2 expression was concentrated in the more mature germ cells. (B) Some OCT4 positive cells were more centrally localised, but no co-localisation of EP2 was seen in these immature cells (noted by neighbouring cells (arrows) exclusively expressing one marker). Dapi (blue) was used for counterstain and scale bars equal 20 microns. Images are representative of staining performed on three separate second trimester tissues.

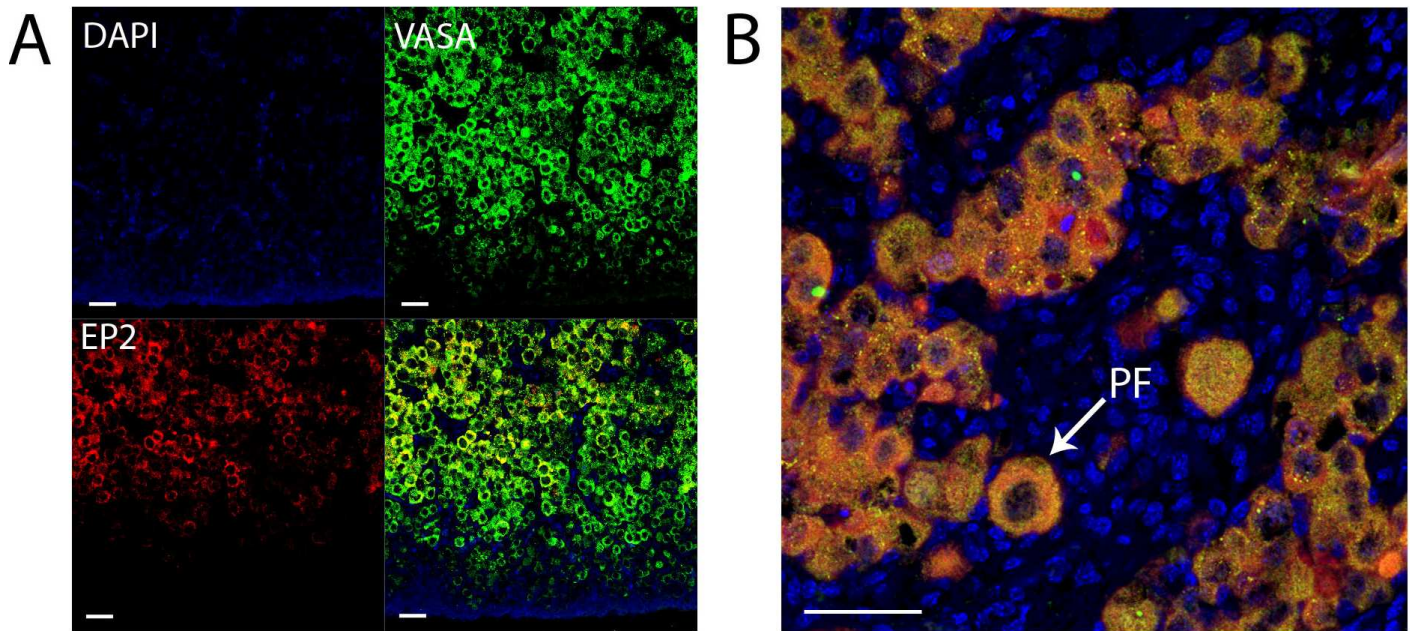


Figure 3.8 *EP2 co-localises with VASA in mature oocytes.*

EP2 (red) and the mature germ cell marker VASA (green) were dual expressed in 18 week human fetal ovarian tissue. (A) VASA expression is germ cell specific but does not stain immature PGCs on the periphery of the ovary. EP2 shows a similar expression pattern but is restricted to even more mature germ cells, as displayed by the more central localisation of expression. (B) Co-localisation of the VASA and EP2 (orange/yellow) in the centre of the ovary demonstrates both proteins are located in mature germ cell nests as well as oocytes within primordial follicles (PF). Dapi (blue) was used for counterstain and scale bars equal 20 microns. Images are representative of staining performed on three separate second trimester tissues.

3.3.7 EP4 is not restricted to primordial germ cells

Co-localisation with EP2 and EP4 demonstrated that the two PGE₂ receptors displayed differing patterns of expression in the human fetal ovary. After confirmation that the EP2 receptor was restricted to maturing oocytes and oocytes within primordial follicles, immunolocalisation was used to further clarify whether EP4 was solely expressed by immature PGCs in the human fetal ovary. The immature marker OCT4 was again utilised for this purpose. PGCs were identified co-expressing both OCT4 (nuclear) and EP4 (membranous) (Figure 3.9A-B); however, co-localisation also revealed EP4 is not germ cell specific, which became more apparent in later gestational tissue, rather EP4 is also expressed by somatic cells and epithelium at the periphery of the ovary (Figure 3.9B). Expression of EP4 was primarily restricted to the edge of the human fetal ovary with less expression seen centrally. These data demonstrate EP4 is not germ cell specific, and is also expressed by interstitial and epithelial cells at the edge of the ovary.

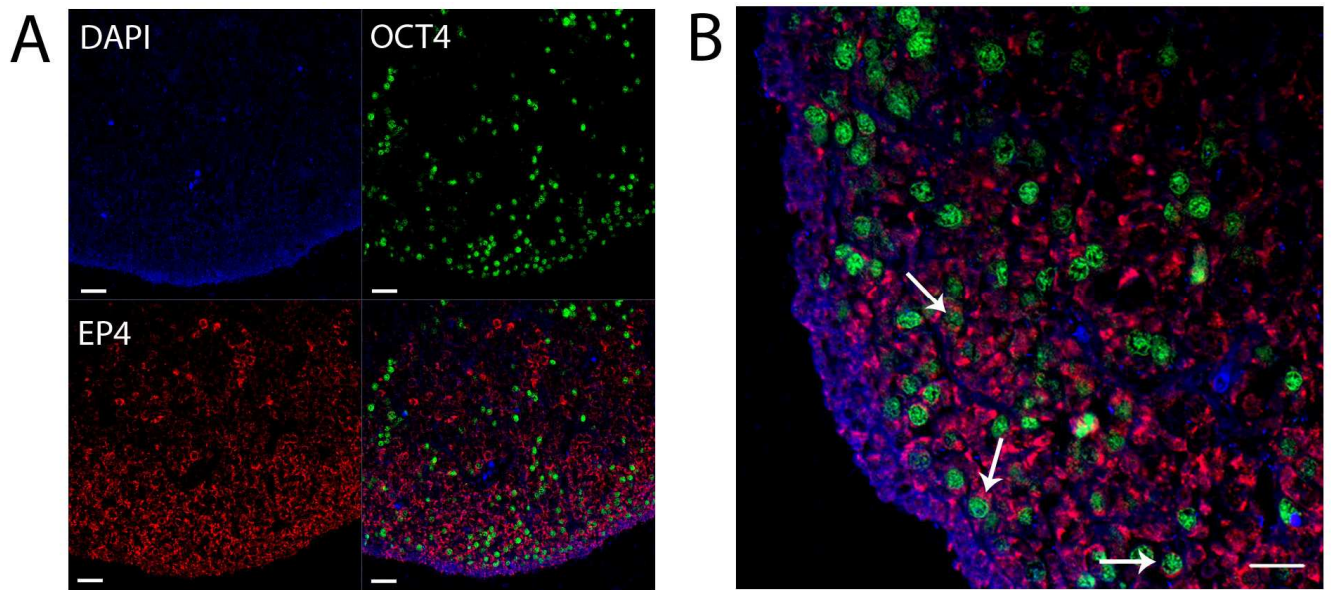


Figure 3.9 *EP4 is not germ cell specific but is more concentrated near the periphery of the ovary.*

EP4 (red) and the immature PGC marker OCT4 (green) were dual expressed in 19 week human fetal ovarian tissue. (A) EP4 is not germ cell-specific and is expressed by the somatic and epithelial cells at the edge of the fetal ovary. (B) EP4 is expressed by some fetal germ cells as co-localisation between OCT4 (nuclear) and EP4 (cytoplasmic) is displayed (white arrows). Dapi (blue) was used for counterstain and scale bars equal 20 microns. Images are representative of staining performed on three separate second trimester tissues.

3.3.8 Determination of PGE₂ function in the human fetal ovary

To determine a possible function for PGE₂ in the human fetal ovary, early second trimester human fetal ovarian cultures were performed in the presence of PGE₂ for 8 hours (n=6), with subsequent qRT-PCR analysis to determine modulation of germ cell genes or known ovarian regulators. Culture tissue was split into three treatment groups; untreated control, indomethacin control (indomethacin was utilised in culture to prevent endogenous PG production, allowing effects of exogenous PG treatment to be investigated), and indomethacin plus PGE₂ treatment.

No change in expression was determined in any of the germ cell markers investigated when comparing indomethacin control against PGE₂ treated tissue (*OCT4* (p=0.62), *VASA* (p=0.87) or *DAZZL* (p=0.63), Figure 3.10A-C). As predicted in the previously discussed array (Jabbour, unpublished) the neurotrophin, *BDNF* was up-regulated by PGE₂ (0.8±0.3 vs 1.3±0.6 relative to *GAPDH*, p=0.004, Figure 3.10D). However, another neurotrophin *NTF5* (which codes for NT4) was not affected by PGE₂ treatment (p=0.22, Figure 4.9E). Another known regulator of ovarian development, *INHBA* (which encodes for the protein Activin A), was also investigated and shown to significantly increase in response to PGE₂ treatment (2.0±0.2 vs 4.2±1.1 x10⁻³ relative to *GAPDH*, p=0.04, Figure 3.10G). In contrast, the two Activin signalling factors *SMAD2* and *SMAD3* were not changed (p=0.26 and 0.25 respectively; Figure 3.10H and I). In addition, the anti-apoptotic factor *MCL-1* was also up-regulated with PGE₂ treatment (3.8±0.2 vs 4.4±0.5 x10⁻² relative to *GAPDH*, p=0.04, Figure 3.10F).

These data demonstrate PGE₂ is capable of regulating expression of *BDNF* and *INHBA*, which are known regulators of ovarian development. PGE₂ also up-regulated *MCL-1*, an anti-apoptotic factor. However, PGE₂ does not modulate germ cell marker expression, the neurotrophin *NTF5*, or the downstream signalling components of Activin.

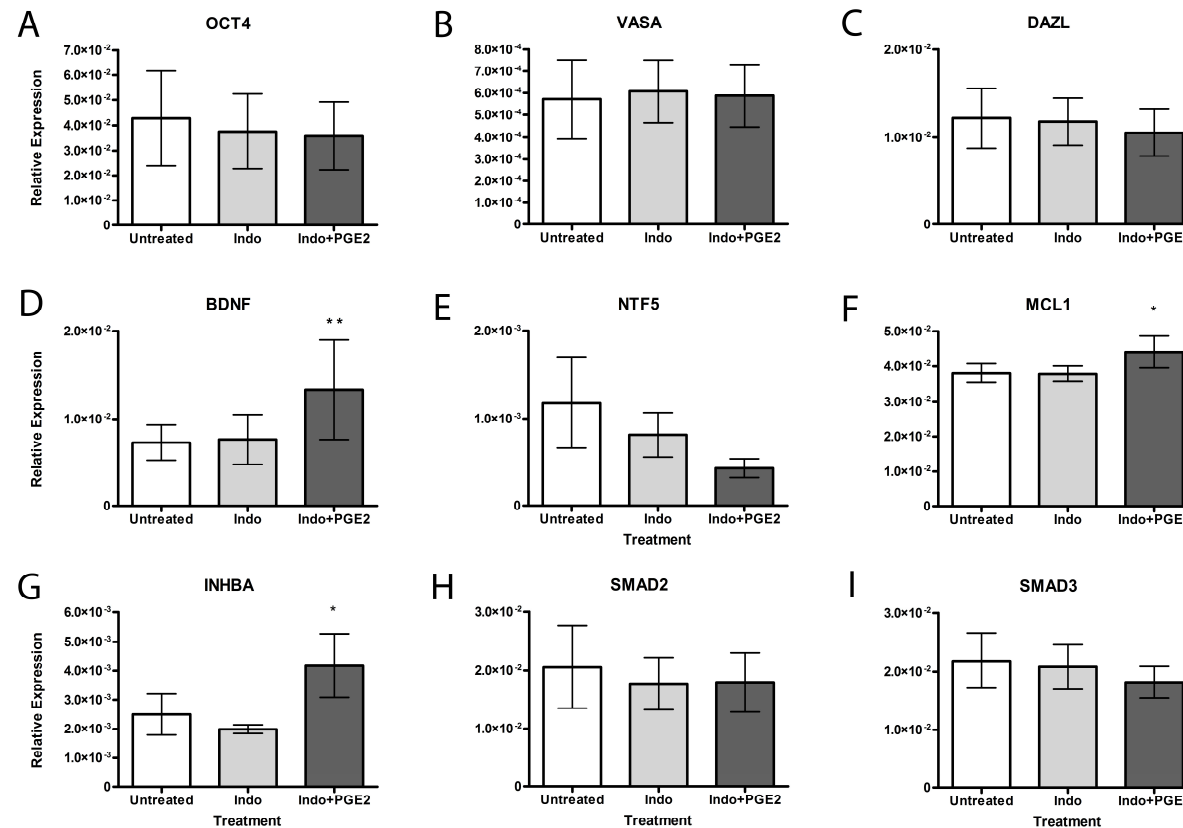


Figure 3.10 qRT-PCR analysis of genomic changes with PGE₂ treatment in the human fetal ovary.

Human fetal ovarian explants were cultured with no treatment (untreated), in the presence of 3 μ g/ml indomethacin (Indo), or indomethacin and 100nM PGE₂ (Indo+PGE₂). No change was seen in the germ cell markers investigated; (A) OCT4, (B) VASA, or (C) DAZL. (D) The neurotrophin BDNF was significantly up-regulated with PGE₂ treatment, but another neurotrophin, NTF5 was not changed. (F) The anti-apoptotic factor MCL-1 was also seen to increase with PGE₂ treatment, as was the TGF- β superfamily member, (G) INHBA. However, neither of the inhibin/activin downstream signalling molecules were altered with PGE₂ treatment (SMAD2 and 3 (H and I)). All data are expressed as relative expression, normalised to the housekeeping gene *GAPDH*. These cultures were performed by Dr. Rosey Bayne.

3.3.9 PGE₂ treatment does not lead to gross changes in apoptosis or proliferation

To further characterise the functional effects of PGE₂ treatment, cultures were repeated in a similar fashion with an extended treatment period of 24 hours and examined for histological changes via the immunohistochemical markers 5-bromo-2'-deoxyuridine (BrdU) which marks proliferation, and cleaved caspase-3 (CC3) which marks apoptosis (n=5). No changes were determined in proliferation (Figure 3.11A and B) of somatic (p=0.81) or germ cells (p=0.98) in the human fetal ovary. Similarly, no changes were seen in the number of cells undergoing programmed cell death (somatic cell apoptosis (p=0.87) and germ cell apoptosis (p=0.60), Figure 3.11C and D). These data demonstrate that treatment with 100 nM PGE₂ for 24 hours does not lead to any gross changes in ovarian cell turnover.

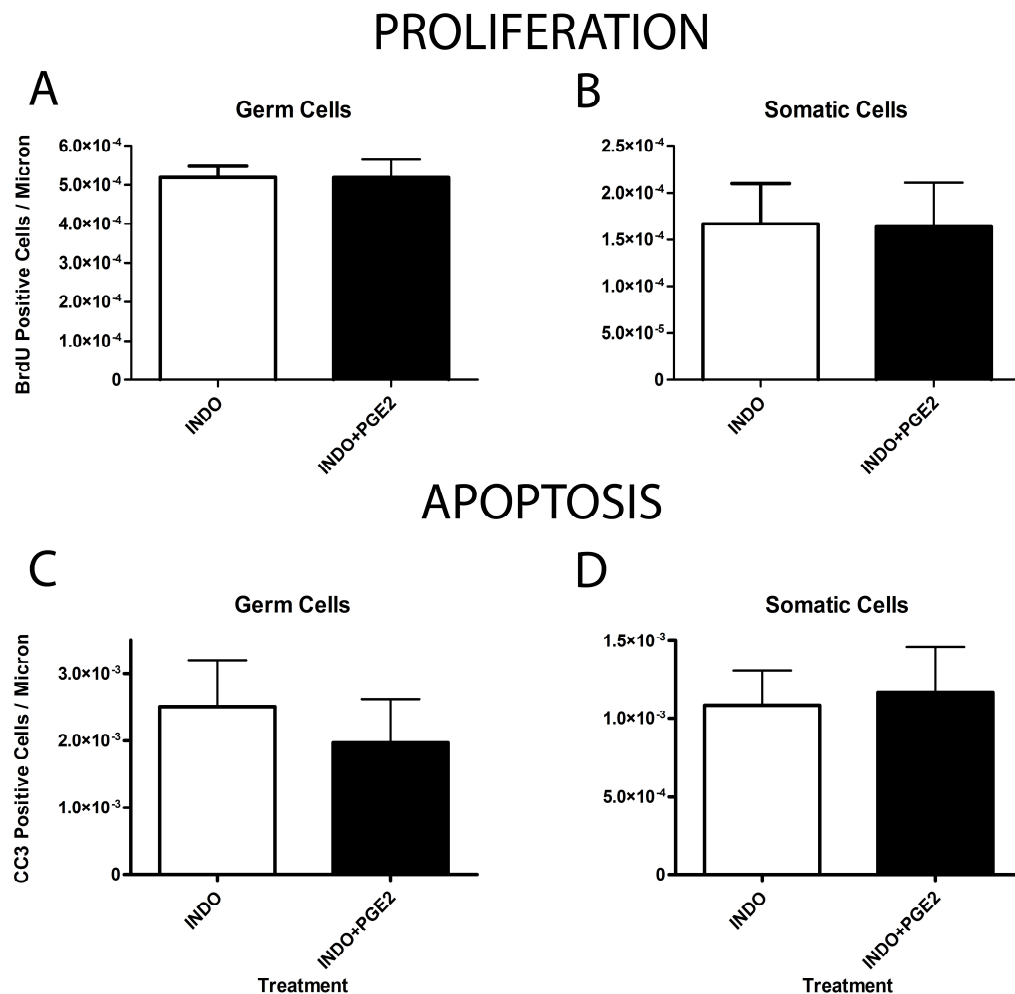


Figure 3.11 No change in proliferation or apoptosis is detected after 24 hour treatment with 100nM PGE₂

Second trimester fetal ovarian tissue (15-17 weeks, n=5), was treated with 3 μ g/ml indomethacin (INDO), or indomethacin and 100nM PGE₂ (INDO+PGE₂) for 24 hours. Proliferation was observed via positive 5-bromo-2'-deoxyuridine (BrdU) staining and was not seen to change in either the (A) germ cell or (B) somatic cell populations. Apoptosis was also assessed via the marker cleaved caspase-3 (CC3) and did not change in (C) germ cells or (D) somatic cells. These data are expressed as positively stained cells per micron of tissue.

3.4 Discussion

Fetal ovarian development and germ cell maturation are vital for adult fertility. PGE₂ has been well-characterised as a potent regulator of ovarian function in the adult (Oates *et al*, 1988a; Oates *et al*, 1988b), but few data exist relating to its function during ovarian development. Additionally, PGE₂ has been identified as a regulator of the neurotrophins in tissue outwith the ovary (Toyomoto *et al*, 2004; Jabbour, unpublished). The neurotrophins are known regulators of early ovarian development leading to the hypothesis that PGE₂ may also play a functional role in the ovary at this time. The data presented here confirm that all precursor enzymes necessary for PGE₂ production (COX1, COX2, and PTGES) are expressed in the human fetal ovary, as are the receptors required for PGE₂ signalling (EP1-4). Furthermore, the expression of several of these components is restricted to the germ cells, denoting PGE₂ is synthesised in the germ cells and can target the germ cells directly in the developing human ovary. Treatment of human fetal ovary with PGE₂ *in vitro* demonstrated increase in expression of germ-cell expressed genes previously identified as important regulators of early ovarian development, providing evidence that PGE₂ may play an important role in developmental signalling in the human fetal ovary.

Expression of two of the precursor enzymes (COX2 and PTGES) required for PGE₂ synthesis was developmentally-regulated. COX2 expression was increased linearly across gestation, with highest expression in late second trimester concomitant with the initiation of primordial follicle formation. PTGES showed a significant drop in expression in early second trimester compared with expression in first and late second trimester, possibly indicating biphasic PGE₂ production in the fetal ovary. Protein of both developmentally-regulated enzymes was found to be exclusively expressed by the fetal germ cells at all gestations (data not shown), revealing germ cells to be the sole site of PGE₂ synthesis in the human fetal ovary. Unlike the other enzymes involved in PGE₂ production, COX1 was consistently expressed across gestation and was localised to the somatic cells at the periphery of the human fetal

ovary. This enhanced role for COX2 over COX1 in ovarian function is supported by rodents deficient for each of the enzymes; COX1^{-/-} females show no disruption of adult ovarian function, whereas COX2^{-/-} females suffer multiple reproductive disruptions including ovulation, fertilisation and implantation (Dinchuk *et al*, 1995; Lim *et al*, 1997). It is also noted that protein expression of COX2 seemed to be heightened in specific germ cells within germ cell nests, together with its heightened expression in late second trimester. This may suggest that COX2 is involved in survival or degradation of specific germ cells leading up to primordial follicle formation.

Expression of the PGE₂ receptors was varied in the human fetal ovary. *EP1*, 2, and 3 showed no significant change in transcript expression across gestation, whereas *EP4* displayed a significant increase similar to that of *COX2*. This pattern was consistent with protein expression, where *EP4* was heightened in later gestations at the periphery of the ovary. This increase in protein expression was not exclusive to the germ cells as first postulated, but rather *EP4* is also expressed by somatic, epithelial and germ cells near the periphery of the ovary. The increase seen in *EP4* and its location may indicate a role in maintenance of the immature PGC population. In contrast, *EP2* was expressed in a more mature subset of oocytes, with little overlap in expression between *EP2* and *EP4* determined. *EP2* was solely expressed by mature germ cells, also positive for VASA, in germ cell nests and oocytes within primordial follicles; this may denote a specific signalling role for *EP2* in mature germ cells. *EP3* was expressed by germ cells and pre-granulosa cells within germ cell nests. Conversely, *EP1* displayed limited expression in the human fetal ovary, with weak staining in blood vessels revealing it is not likely to be involved in fetal ovarian/germ cell development. Based upon these findings it is likely that PGE₂ action in the human fetal ovary is via *EP2*, 3, or 4. Distinct expression of each of these receptors provides evidence for multiple roles for PGE₂ as it interacts with the differing receptors during ovarian development and germ cell maturation. Of the *EP* receptors, *EP2* is the only one to be shown to be essential in adult ovarian function, as loss of *EP2* function in a murine model resulted in impaired ovulation (Hizaki *et al*, 1999; Kennedy *et al*, 1999; Tilley *et al*, 1999). However, it is probable that PGE₂

action in the fetal ovary is orchestrated via multiple receptors to exert differing effects on distinct subsets of germ cells. With PGE₂ synthesised in germ cells, receptor localisation demonstrates this PGE₂ function can be via autocrine (germ cell) or paracrine (somatic cell) action.

It is possible the developmental changes in mRNA expression of the enzymes and receptors are a result of changes in the tissue composition as the fetal ovary develops, rather than increased expression as a result of increased PGE₂ signalling. As discussed in the introduction, in the human fetal ovary the germ cells proliferate greatly between first and second trimester, increasing their proportion compared to the somatic environment. This may account for some of the increase in expression seen in *COX2*, *PTGES* and *EP4*. However, if this were the only cause for increases determined, expression of *PTGES* should also increase. In addition, as expression of the germ-cell specific receptor *EP2* is not increased in a significant fashion and conversely the somatic-specific enzyme *COX1* is not significantly decreased with gestation, it does not appear that the significant changes in expression levels can be solely due to changes in ovarian composition.

Subsequent culture analysis partially illuminates PGE₂ function during early development. As the PGE₂ receptors were expressed primarily by germ cells in the human fetal ovary, tissue was assessed for any changes in expression of germ cell markers (*OCT4*, *VASA*, and *DAZL*), whose expression is also associated with differing stages of germ cell development (Anderson *et al*, 2007). No significant changes were seen that might suggest a change in germ cell development, which provides further evidence for an upstream effect on germ cell growth factors rather than a direct action on germ cells survival. However, it is possible the short timecourse of 8 hours was not long enough to determine developmental effects.

As speculated, the neurotrophin *BDNF* was up-regulated by PGE₂ treatment. However, another neurotrophin *NTF5* was not affected by PGE₂ treatment. The receptor for these neurotrophins, the TrkB receptor, has been well characterized as an important mediator of development in the mammalian ovary (Dissen *et al*, 1995; Spears *et al*, 2003; Paredes *et al*, 2004; Childs *et al*, 2010a). Both BDNF and NT4

are expressed primarily in the somatic cells in the developing human ovary (Coutts *et al*, 2008; Childs *et al*, 2010a); however, *BDNF* expression is also present in the germ cells at later gestations. Given that PGE₂ receptors are primarily expressed by the germ cells, it is possible this difference in regulation is due to *BDNF* mRNA up-regulation specifically in the germ cells, which may explain the lack of effect on *NTF5*.

Supporting this germ cell specific effect hypothesis, is the up-regulation of *MCL-1* and *INHBA*, which are also expressed solely by the larger, more mature germ cells, including oocytes within primordial follicles (Hartley *et al*, 2002; Martins da Silva *et al*, 2004). *INHBA* is another known regulator of human fetal ovarian development, which exhibits increased transcript levels in late second trimester (Martins da Silva *et al*, 2004) and may regulate germ cell development via regulation of kit ligand/c-KIT expression (Coutts *et al*, 2008; Childs *et al*, 2010a). As PGE₂ is able to up-regulate *INHBA* expression, it is possible it plays an up-stream role in this regulation. *MCL-1*, an anti-apoptotic factor (Kozopas *et al*, 1993), was also up-regulated by PGE₂ treatment. This up-regulation may be a direct action or possibly secondary to the up-regulation of *INHBA*, as *MCL-1* can be regulated by Activin in other systems (Fukuchi *et al*, 2001). In contrast, other downstream targets of Activin action, SMAD2 and 3, were not affected by PGE₂ treatment, but as with *NTF5*, these factors are located in the somatic cell population.

In order to further determine the functional effects of these expression changes, the PGE₂ cultures were repeated with an extended culture period of 24 hours. No changes were determined in the rate of proliferation or apoptosis in either somatic or germ cell populations. This observation and the inability of PGE₂ to modulate expression of germ cell genes suggest that PGE₂ may not have a direct role in germ cell survival, rather regulating other factors in ovarian development, although the lack of functional changes in histology may also be due to the short duration of the culture (24 hours). Further investigation, using either an *in vivo* model, such as the mouse, or an extended *in vitro* culture system capable of sustaining tissue survival for extended periods of time would be beneficial for determining PGE₂ function.

In conclusion, the necessary components for PGE₂ signalling are present in the fetal ovary, and treatment with PGE₂ can increase transcript levels for germ-cell specific factors known to be important for oocyte survival and maturation. These data provide novel evidence for PGE₂ as a regulator of early human ovarian signalling and thereby germ cell development. Future research should establish the direct function PGE₂ may play during germ cell development.

Chapter 4

Effects of maternal paracetamol usage on fetal ovarian development

Chapter 4. Effects of maternal paracetamol usage on fetal ovarian development

4.1 Introduction

Studies in the human fetal ovary determined a possible function for PGE₂ in regulation of oocyte survival and proliferation, but were unable to determine its mechanism of action; therefore, it was determined a longer duration, in vivo model of PG disruption would be beneficial in order to investigate further PG function (specifically PGE₂) during fetal ovarian development. Maternal administration of paracetamol (acetaminophen) during pregnancy in a rodent model was utilised for this purpose, as treatment with PGE₂ would likely induce early parturition (Kelly *et al*, 2009), administration of other PG inhibitors (indomethacin, NSAIDs, etc) causes maternal morbidity (Wilcox *et al*, 1997; Sigthorsson *et al*, 2000), and a model of maternal exposure to paracetamol is clinically relevant.

More than 50% of women in the Western world use analgesics during pregnancy, with paracetamol being most widely used (Werler *et al*, 2005). Paracetamol is similar to the NSAID family of analgesics, with both drug types functioning via the inhibition of the COX enzymes to prevent inflammatory signalling. However paracetamol is a weak anti-inflammatory with poor anti-platelet activity compared to the NSAIDs (Lages & Weiss, 1989; Niemi *et al*, 2000). This difference is likely due to differing mechanisms of action. NSAIDs directly inhibit the COX enzymes both in the central nervous system (CNS) and peripheral systems (Ayoub *et al*, 2006). Conversely, paracetamol, despite being on the market for over 50 years, does not have a well-characterised mechanism of action, although it has been established it interacts with the COX enzymes (Graham & Scott, 2005). It was briefly hypothesised that paracetamol functioned via inhibition of a third, yet to be characterised COX enzyme (COX3) (Chandrasekharan *et al*, 2002) but this hypothesis has since been rejected (Dinchuk *et al*, 2003; Schwab *et al*, 2003) (Schwab, 2003). Recent evidence suggests the primary target of paracetamol action in the human is COX2, as it exhibits comparable COX2 inhibition to other NSAIDs and COX2-specific inhibitors, but is unable to suppress COX1 to therapeutic levels

comparable to the NSAIDs (Hinz *et al*, 2008). There may also be other targets of paracetamol action, and its direct mechanism of inhibiting COX2 remains unknown.

Specific COX2 inhibitors, including paracetamol, are commonly prescribed for chronic pain and/or inflammation management, as COX2 specific inhibitors do not induce gastrointestinal bleeding, which is a side effect of long-term inhibition of COX1 in NSAIDs (Wilcox *et al*, 1997; Sigthorsson *et al*, 2000). It is also thought COX2 inhibitors are less likely to cause renal complications when compared to traditional NSAIDs (Zhao *et al*, 2001; Whelton *et al*, 2002). However, COX2 inhibitors have been shown to heighten risk of cardiovascular complications with long term use (Bombardier, 2002; Bresalier *et al*, 2005).

Despite this, paracetamol has been considered safe, with no reported fetotoxic effects when taken within the therapeutic range (Rathmell *et al*, 1997). However, recent studies from Denmark have disputed the safety of prenatal exposure to analgesics, suggesting that maternal usage of these drugs, including paracetamol, results in increased risk of cryptorchidism in male offspring (Kristensen *et al*, 2011). This was determined via a meta-study of maternal usage of analgesics; paracetamol and NSAIDs (non-steroidal anti-inflammatory drugs; aspirin and ibuprofen), noting duration of use and what point in gestation the treatment was taken. This study determined use of analgesics was associated with congenital cryptorchidism in a dose-dependent manner, with increased risk in mothers who used analgesics during second trimester. These data were further supported by a rodent model that demonstrated paracetamol produced anti-androgenic effects in offspring leading to impaired masculinisation (as demonstrated by reduced ano-genital distance; (Kristensen *et al*, 2011)).

As previously discussed COX enzymes, which are targeted by paracetamol and NSAIDs, synthesise PGs and other inflammatory mediators. Outwith the Kristensen *et al.* study, historical literature from Gupta and colleagues has also demonstrated inhibition of the Cox enzymes and indeed direct inhibition of the Pgs is able to disrupt male development in rodents (Gupta & Goldman, 1986; Gupta, 1989). However, the effect of maternal analgesic usage on female development has not been investigated.

Current knowledge of PG involvement in gonad development is limited. PGD₂ is thought to be involved in early sex determination, and based upon data gathered in the previous chapter, it is postulated that PGE₂ plays a regulatory role during ovarian development. Inhibition of PG synthesis by analgesics during pregnancy would affect these pathways and might lead to disruption of gonad development in offspring. To test this hypothesis, as well as further examine the function of PGE₂ during fetal ovarian development, the rat model used in the Danish study was duplicated (Kristensen *et al.*, 2011). This model utilises maternal gavage (oral administration) also allowing the study to remain clinically relevant to human administration of analgesics during pregnancy. Resulting female pups were examined for gross morphological and gonadal differences compared to pups exposed to vehicle control (corn oil). Further investigation of the male pups and testis development was also investigated by collaborators, but will not be discussed in this chapter.

4.2 Materials and Methods

Tissue collection and dissection

Pregnant Wistar rats were either treated with 350 mg/kg paracetamol in oil for 7 days of gestation or oil control alone, from day e13.5 to e20.5. Fetal rat ovaries were collected at embryonic day (e)21.5 of gestation. In a second series of studies, paracetamol treatment was the same but with exposure for only 3 days with ovaries collected at day e17.5. 5 litters of each treatment group were analysed in the following experiments (with at least 3 animals per litter analysed). Full details are in Section 2.2.

Gross morphological measurements

Body mass and ano-genital distance (AGD) were measured at dissection using a micro-balance (Sartorius Handy model #110) and digital callipers (Faithfull Tools). Body mass was measured before decapitation to detect possible systemic changes. AGD was measured from the start of the anus to the start of the phallus in both sexes as an index of masculinisation (Figure 4.1). Scales and calipers were re-calibrated before use.

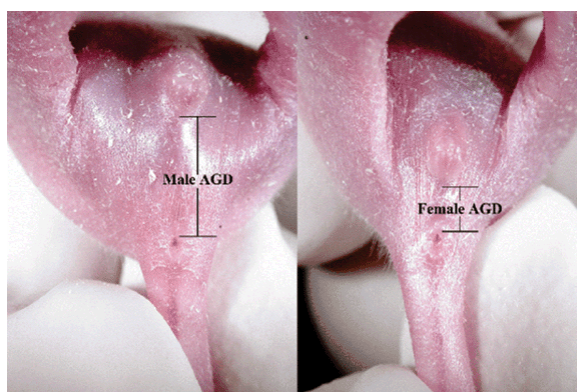


Figure 4.1 *Ano-genital distance measurement*

Ano-genital distance (AGD) was measured as indicated above, with a clear difference between male and female animals. AGD was utilised as an early indicator of disruption of masculinisation (Ostby & Gray, 2004)

AGD was also adjusted for body mass, as AGD changes in proportion to body size. The equation is as described below and the adjusted measurement referred to as anogenital index (AGI).

$$\text{AGI} = \text{AGD (mm)} / \text{body mass}^{1/3} \text{ (grams)}$$

Immunohistochemistry

In order to determine if rodent expression of Pge₂ factors was similar to that of the human fetal ovary, Cox1, Cox2, Ptges, and Ep1-4 were localised in the rat ovary using the same concentrations of primary antibody as in the human. Further to determine changes in germ cell number, both Tra-98 and Vasa staining were utilised, with additional staining for proliferation marker phosphohistone-H3 (PHH3) and apoptosis marker cleaved caspase-3 (CC3) to identify any changes in ovarian cell turnover. Details of immunohistochemical protocols can be found in Section 2.8.

Stereology

All stereology was performed using the equipment described in Section 2.11.3. All counts were performed blind to prevent inadvertent bias.

Ovarian volumes

Fetal rat ovaries were serial sectioned, with 2 sections placed on each slide. Every tenth slide was stained with hematoxylin and eosin (as in Section 2.7) and the ovarian area measured. An average ovarian area and the number of slides containing complete ovarian sections was then used to extrapolate volume using the equation below and as depicted in Figure 4.2.

$$\text{ovarian volume} = \text{average ovarian area} \times (\text{number of slides containing ovary} \times 10 \mu\text{m})$$

(Each section is 5 μm , and each slide contains two sections making each slide 10 μm).

This calculation is based upon Cavalieri's principle, which postulates the area of 2D sections multiplied by the distance from end to end of an object is an accurate calculation for volume of the object, regardless of shape. This principle has been verified as an accurate way to discern tissue volume, as long as the sections examined are of equal interval (Mayhew & Olsen, 1991).

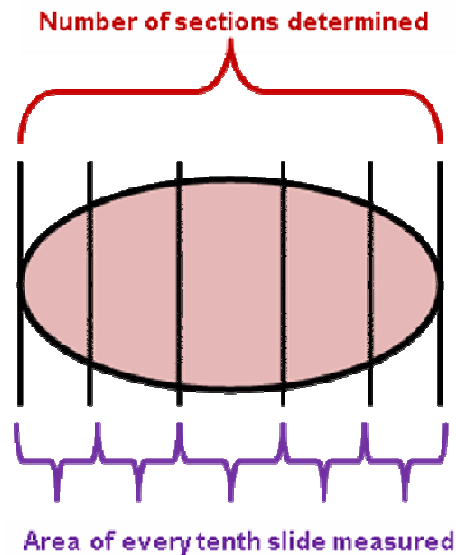


Figure 4.2 Schematic of determination of ovarian volume.

Fetal rat ovaries were serial sectioned. Area of every tenth slide was determined using image analysis and the area averaged before multiplying by the depth of ovary as determined by number of slides and thickness of the sections on the slides.

Germ cells per area

The germ cell marker Tra-98 was used to mark germ cells in the fetal rat ovary, and stereology was performed to count number of germ cells using two slides per animal (one from the centre of the tissue as determined from ovarian area, and another at least fifty microns from the centre). The number of germ cells quantified was then adjusted for ovarian area determined from the same section and presented as germ cells per micron². A figure depicting this analysis can be found in Section 2.11.

Germ cell nuclear diameter

Germ cell nuclear diameter (GCND) can be used as an index of oögonia/oocyte maturation, with more mature germ cells having larger nuclear diameters. Germ cell nuclear diameter was measured using the ‘nucleator’ function of the above software, which tri-sects the germ cell and each of 6 radii are measured. These radii are then averaged to provide an accurate measurement of nuclear diameter of the cell. Fifty germ cells per section were randomly measured in this fashion, and two sections (the same slides were utilised for both germ cell number quantification and GCND measurement) from each animal were quantified. Some of the paracetamol treated animals did not have 50 germ cells in a section. In these cases, all germ cells were measured.

Apoptosis

Apoptosis was measured via the marker CC3, as in the previous chapter. CC3 positive cells were counted and adjusted for ovarian area and presented as apoptotic cells per micron².

Proliferation

Proliferation was measured via the marker PHH3, similarly to the protocol used in the previous chapter for BrdU. PHH3 positive cells were counted and adjusted for ovarian area and presented as proliferating cells per micron².

Statistical Analysis

Gross and stereological measurements were analysed with GraphPad Prism version 4 (GraphPad Software Inc). Student's unpaired t-test was utilised for determination of significant changes between treatment groups, following analysis of each measurement for normality utilising the Kolmogorov-Smirnov test.

Data were analysed both on an individual basis and as litter average. This was performed by averaging the individual animal data for each animal from the same litter/dam.

4.3 Results

Fetal rat ovaries were collected after paracetamol or control treatment for 7 days of pregnancy at e21.5 gestation, and the following analyses were performed. Gross morphological data presented (body mass, AGD, and AGI) is based upon all female animals collected (n=7 litters for both treatment, consisting of 35 control pups and 36 treated pups). The subsequent stereological data was only performed on a subset of female animals chosen randomly, from 5 litters from both control and treated groups examined and at least 3 animals from each litter analysed (n=16 control animals and 16 treated animals). Only 5 of the 7 litters obtained were chosen for further stereological analysis. One litter from each of the control and treated groups was omitted for having either fewer than 3 female pups or having an abnormally small litter. All data were analysed and presented both as individual animal data and litter mean data to reveal any possible 'litter effects' which can be caused if animals from one or more litter are above or below average, resulting in skewed data.

4.3.1 Fetal body mass is not altered by paracetamol exposure

Body mass was taken before decapitation of all fetal rats collected. Although there was a non-significant trend for paracetamol rats to be heavier when analysed as individual animals ($p=0.23$, Figure 4.3A), this trend was not seen when animals were analysed by litter means ($p=0.73$, Figure 4.3B). These data establish there are no major changes in pup body mass with maternal usage of paracetamol.

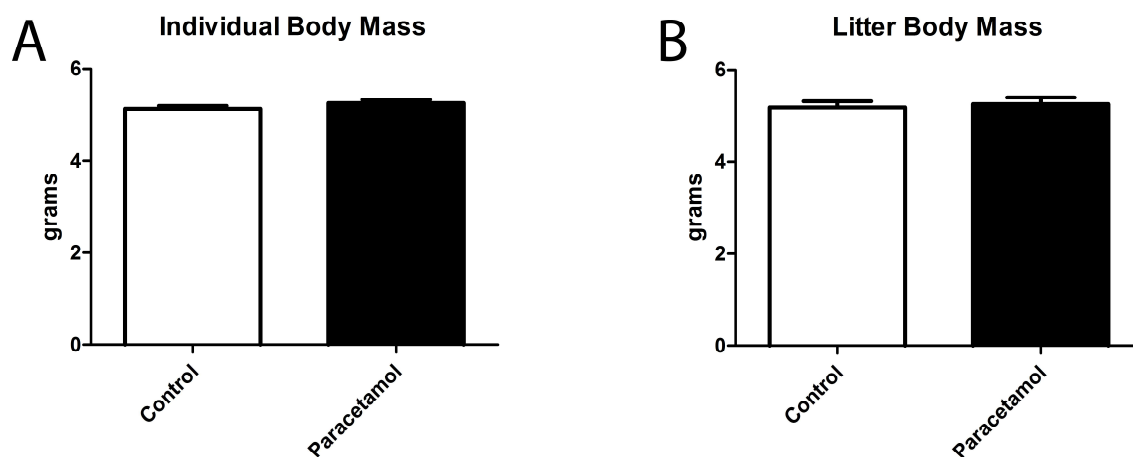


Figure 4.3 *Female pup body mass does not change after fetal paracetamol exposure.*

Body mass was taken for e21.5 fetal female rats treated with 350mg/kg paracetamol (paracetamol) for 7 days of gestation or vehicle control (control). (A) No change was determined in body weight between paracetamol exposed and control individuals. (B) This is consistent when analysed as litter mean, with no significant difference seen between treatment groups.

4.3.2 Masculinisation as determined by AGD and AGI is not changed with maternal usage of paracetamol

AGD is classically used as an early indicator of masculinisation during fetal development (Edwards, 2006). As data from previous studies suggest paracetamol exposure may affect early androgen signalling thus affecting male development, both AGD and AGI were examined. Analysis of individual animal's AGD resulted in a trend for increased AGD in paracetamol exposed animals as compared to control ($p=0.06$), suggesting treated animals may have increased androgenic signalling compared to control animals (Figure 4.4A). However, this trend was lost when analysed using litter mean data ($p=0.61$, Figure 4.4B). As a slight change was detected in body mass, AGI was also utilised and confirmed there was no change in masculinisation of the female pups on both the individual basis or by litter mean data ($p=0.10$ and $p=0.67$, Figure 4.5A and B respectively).

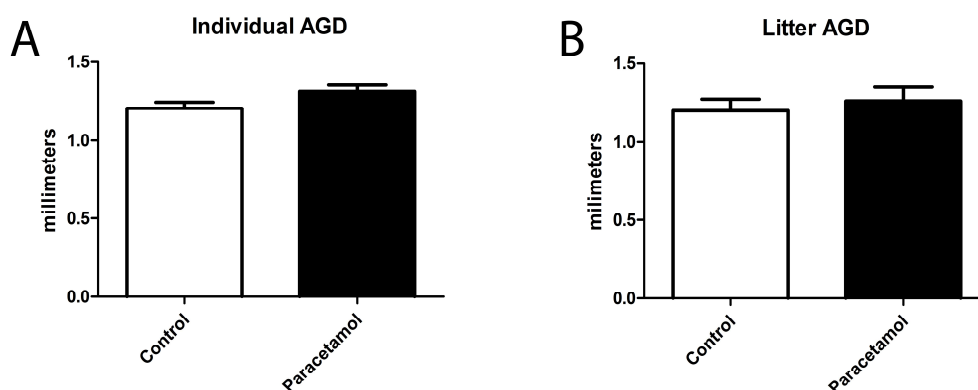


Figure 4.4 *Ano-genital distance is not affected in female pups exposed to paracetamol.*

AGD of e21.5 fetal female rats was measured in both treated (350mg/kg paracetamol for 7 days of gestation (paracetamol)) and control (control) animals. (A) A trend for increased AGD was seen in paracetamol treated animals but was not deemed significant. (B) This trend was not seen when data was analysed using litter means suggesting individual animal variance may have been responsible for the trend seen when analysed as individual animals.

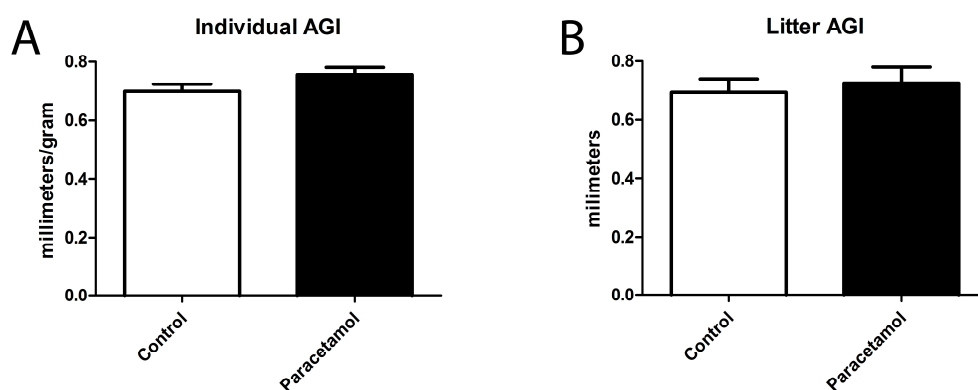


Figure 4.5 *Ano-genital index is not affected in female pups exposed to paracetamol.*

AGI of e21.5 fetal female rats was measured in both treated (350mg/kg paracetamol for 7 days of gestation (paracetamol)) and control (control) animals. (A) No change was seen in AGI when analysed using individual animal measurements or (B) using litter mean measurements.

4.3.3 Ovaries from paracetamol treated pups are significantly smaller than control ovaries

Fetal rat ovaries at e21.5 are relatively small compared to fetal rat testes or human fetal ovaries, and are enclosed in a thin layer of tissue referred to as the ovarian capsule. These two features restricted initial measurement of ovarian mass, as removal of the capsule increased risk of damage to the ovarian tissue underneath and acquiring an accurate measurement of such small tissue was difficult. Therefore, ovaries were removed and fixed with capsule intact and further examination was performed on serial sections of tissue. Initial investigation of the ovaries was performed using the germ cell markers Tra-98 and Vasa. Visual evaluation of morphology indicated there might be differences in both size and number of germ cells in the ovaries of paracetamol exposed tissue compared to control tissue (Figure 4.6). Therefore further quantification was performed.

Ovarian volume was measured via stereology to determine potential differences in ovarian size between treatment groups. Quantification determined the ovaries of paracetamol treated rats were smaller than control ovaries when analysed on both an individual (2.6 ± 0.4 vs $4.2 \pm 0.3 \times 10^7$ micron³, $p=0.0017$, Figure 4.7A) and litter mean basis (2.7 ± 0.5 vs $4.3 \pm 0.3 \times 10^7$ micron³, $p=0.03$, Figure 4.7B). These data suggest paracetamol exposure *in utero* effects ovarian size. This decrease in mass is not seen in body weight, suggesting the difference may be due to a loss of cells within the ovary.

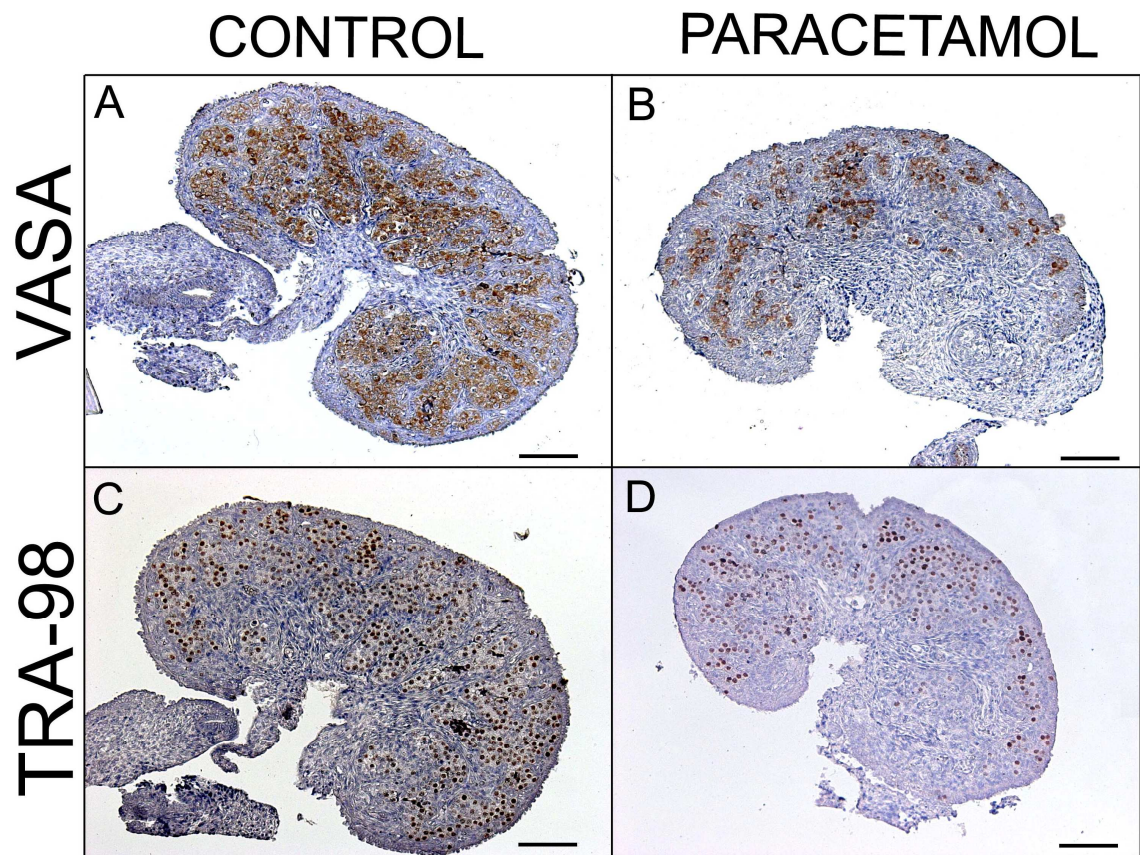


Figure 4.6 Morphological comparison of paracetamol exposed ovaries to control ovaries.

Serial sections from control (A and C) and paracetamol exposed (B and D) e21.5 fetal rat ovaries. Immunolocalisation (brown) for cytoplasmic germ cell marker Vasa (A and B) and nuclear marker Tra-98 (C and D) demonstrating visual observations of smaller ovarian size as well as fewer germ cells in the paracetamol exposed ovaries. Scale bars equal 50 microns.

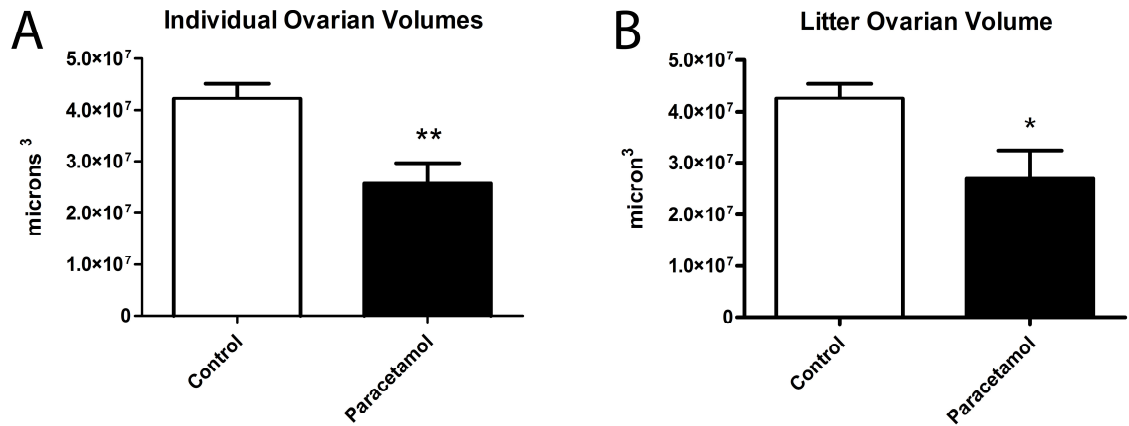


Figure 4.7 Ovarian volumes from e21.5 fetal rats.

Fetal ovarian volumes were determined using stereological methods. (A) Paracetamol treated pups (paracetamol) had significantly smaller ovaries than control animals (control) when analysed by individual animals (n=16 control and treated animals, **= $p < 0.01$). (B) Paracetamol treated ovaries also retained significance when analysed as litter means (n=5 litters for both treated and control, *= $p < 0.05$).

4.3.4 Fetal exposure to maternal paracetamol results in a decreased number of germ cells

As it was hypothesised the decrease in ovarian volume might be the result of a loss of a specific cell type within the ovary and based upon visual observation of decreased germ cell staining, germ cell number was quantified in control and paracetamol treated ovaries. Germ cell counts were adjusted for ovarian area as paracetamol ovaries were deemed to be significantly smaller, in order to reveal if germ cell number was independently altered with fetal paracetamol exposure. Paracetamol treated ovaries displayed a significant reduction in germ cells per micron² of ovary in comparison to controls when analysed as individual animals (1.0 ± 0.1 vs $1.8 \pm 0.2 \times 10^{-3}$, $p=0.004$, Figure 4.8A). When analysed as litter means the loss of germ cells remained consistently significant between paracetamol and control litters (1.0 ± 0.1 vs $1.8 \pm 0.2 \times 10^{-3}$, $p=0.01$, Figure 4.8B). These data suggest factor/s altered by paracetamol exposure lead to germ cell loss or possibly decreased proliferation in fetally exposed ovaries.

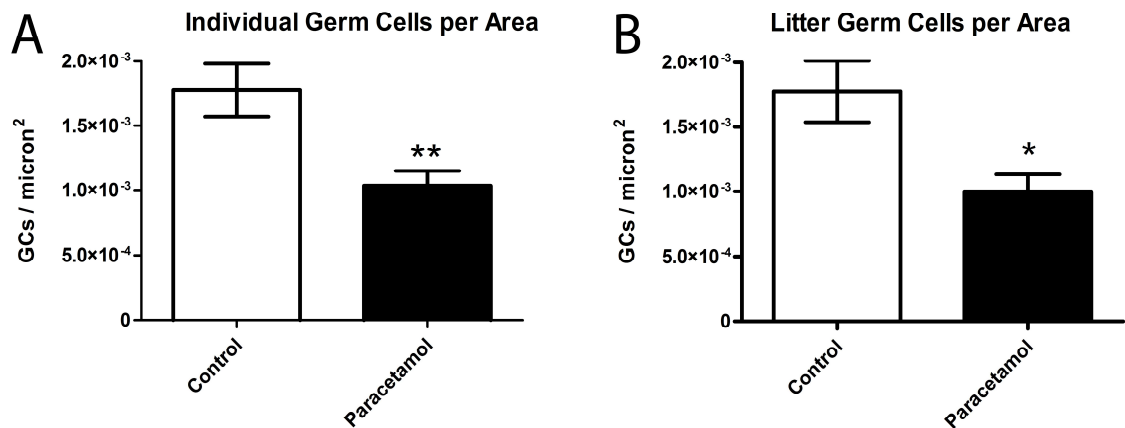


Figure 4.8 *Ovarian germ cell number is decreased with maternal usage of paracetamol.*

Germ cell number was determined using the nuclear germ cell marker Tra-98 via stereological methods and adjusted for ovarian size. (A) Ovaries from paracetamol treated pups (paracetamol) had significantly fewer germ cells per micron² when compared to control ovaries (control) (n=16 for both groups, **=p<0.01). (B) This reduction in germ cell number was also seen when germ cell number was analysed using litter means (n=5 for both groups, *=p<0.05).

4.3.5 Reason for reduction in germ cell number is not apparent at e21.5.

In order to identify a possible mechanism for germ cell loss in paracetamol treated ovaries, the rate of apoptosis and proliferation in treated and control ovaries was assessed. Rate of programmed cell death, as determined by the apoptotic marker CC3, was not significantly different between control and paracetamol exposed ovaries on an individual or litter basis ($p=0.54$ and 0.21 , Figure 4.9A and B respectively). Additionally, no significant change was seen in proliferation when using the mitotic marker PHH3, on either an individual or a litter mean basis ($p=0.22$ and 0.25 , Figure 4.10A and B respectively). These rates are demonstrated as a percentage of positively stained (CC3 (Figure 4.9C-D) or PHH3 cells (Figure 4.10C-D)) compared to total germ cell number (as collected from previous data). These data determine that paracetamol exposure is not affecting normal ovarian cell turnover at e21.5, although the decrease in germ cell number may be a result of a developmental arrest.

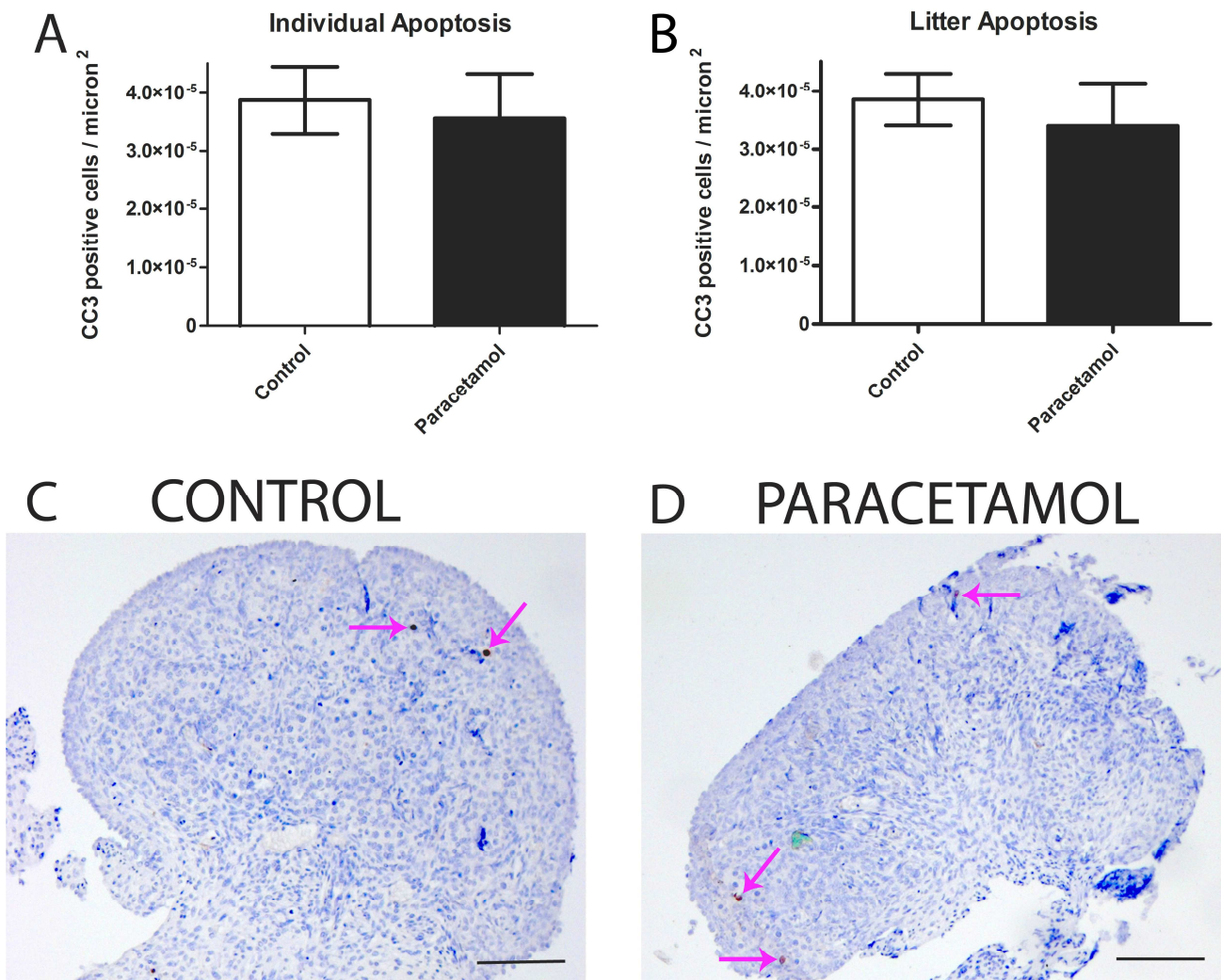


Figure 4.9 *Germ cell reduction in paracetamol ovaries is not the result of increased apoptosis.*

Rates of germ cell apoptosis were determined using the apoptotic marker cleaved capsase-3 (CC3) via stereological methods and adjusted for total number of germ cells, in order to demonstrate the proportion of CC3 positive germ cells per animal or litter. (A) No change was seen in ovarian apoptosis with fetal paracetamol exposure when examining changes in individual animals (n=16 animals per treatment). (B) This finding was confirmed using litter means, however there was a trend of increased apoptosis in paracetamol treated pups (n=5 litters per treatment). (C) Control and (D) paracetamol treated ovaries stained for CC3 (pink arrows). Scale bars equal 50 microns.

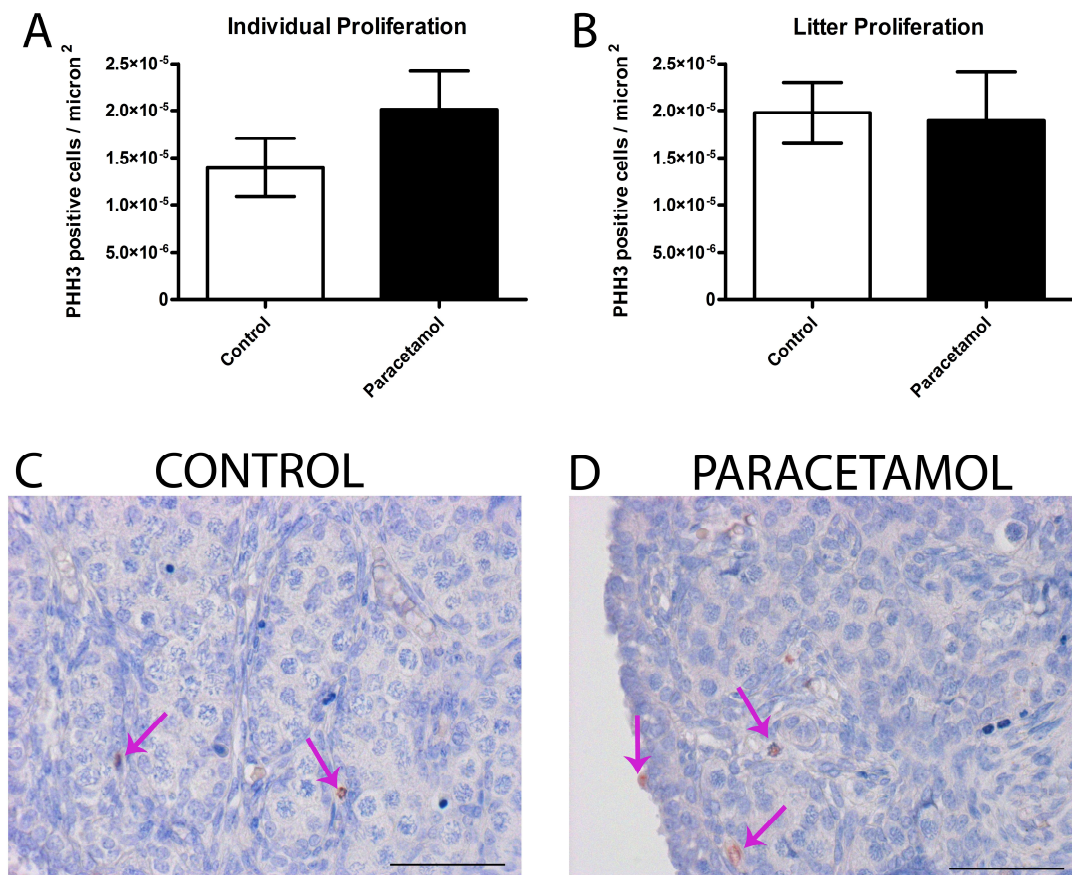


Figure 4.10 Germ cell reduction in paracetamol ovaries is not the result of decreased proliferation.

Proliferation rate was examined using the marker phospho-histone H3 (PHH3) via stereological methods and adjusted for total number of germ cells. The number of PHH3 germ cells per area was then adjusted for total germ cell number to demonstrate the proportion of PHH3 positive germ cells per animal or litter. (A) A trend was seen for more proliferation in individual paracetamol exposed ovaries when compared to control animals but was not significant (n=16 ovaries per treatment). (B) This trend was also seen using litter mean but was also not significant (n=5 litter per treatment). (C) Control and (D) paracetamol treated ovaries stained for PHH3 (pink arrows). Scale bars equal 100 microns.

4.3.6 Fetal paracetamol exposure delays germ cell progression and may affect germ cell synchronicity in the rat ovary

GCND was examined as a measurement of germ cell maturity in both control and treated ovaries, in order to distinguish if paracetamol exposure had any effects on germ cell development. When individual animal GCND means were calculated, germ cells from paracetamol animals were found to have significantly smaller GCND ie be less mature than those from control ovaries (7.4 ± 0.1 vs 6.8 ± 0.2 microns, $p=0.03$, Figure 4.11A). However, when GCNDs were analysed as a litter mean, significance was lost, although the trend remained ($p=0.07$, Figure 4.11B). The rat ovary is comparatively synchronous at e21.5, composed of germ cell nests of roughly the same developmental stage; therefore, GCND data was further analysed to determine the proportion of cells at each diameter to detect subtle changes in maturation and changes in synchronicity.

Analysis of the total population of germ cell measured for each treatment determined there was a significant difference in the distribution of development between control and paracetamol treated germ cells, with a larger population of smaller, immature germ cells in the paracetamol ovaries when compared with control (7.4 ± 0.03 vs 7.0 ± 0.04 microns, $n=1385$ and 1166 , $p=0.0001$, Figure 4.11C). In addition, paracetamol ovaries displayed a lack of synchronicity, compared with control germ cells, of which ~80% remained within a variance of only $3 \mu\text{m}$ compared to a $4 \mu\text{m}$ variance in the same proportion of cells from paracetamol exposed ovaries. However, the paracetamol exposed germ cells were still able to reach the same maturity levels as seen in control germ cells (albeit fewer cells reached these stages), demonstrating a complete arrest of development was not occurring in paracetamol exposed ovaries, rather a developmental delay.

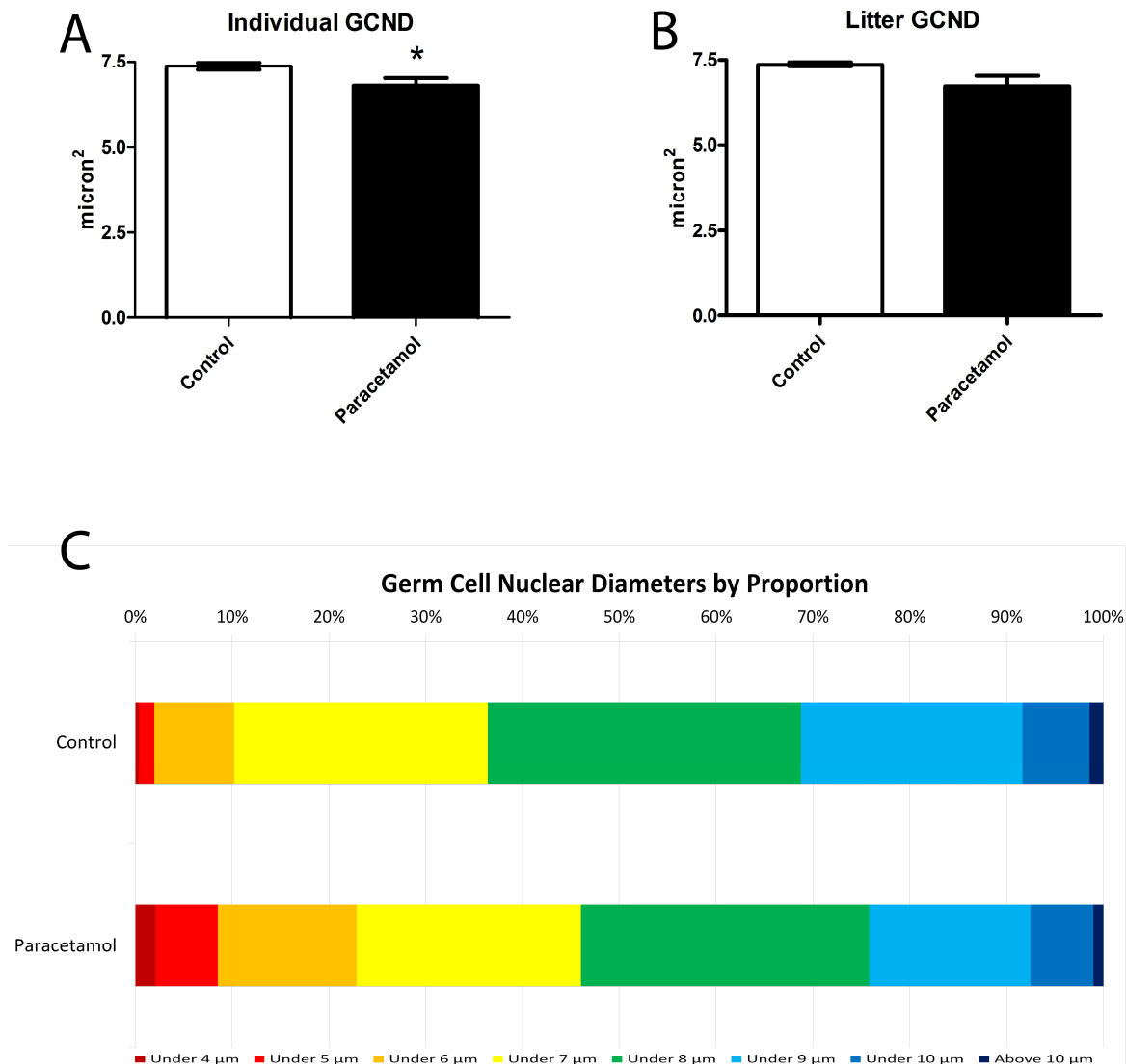


Figure 4.11 Development of germ cells in paracetamol exposed ovaries is delayed and less synchronous when compared to control germ cells.

Germ cell nuclear diameter (GCND) was determined using the nuclear germ cell marker Tra-98 via stereological methods. (A) A significant reduction in germ cell nuclear diameter can be seen upon comparison of individual animal GCND means (*= $p < 0.05$, $n=16$ control and treated animals). (B) This trend was consistent when comparing litter mean data, but was not significant ($n=5$ litters per group). (C) Total germ cell population from all animals was further analysed to determine subtle changes in maturation and changes in synchronicity ($n=1385$ control germ cells and 1166 paracetamol exposed germ cells).

4.3.7 Paracetamol effects on fetal rats at e17.5

Although we determined exposure to paracetamol over 7 days *in utero* affects fetal rat ovaries when examined at e21.5, no clear mechanism for these effects was determined. It was postulated the changes in ovarian size, germ cell number, and GCND may be the result of paracetamol effects earlier in gestation. In order to examine possible changes in apoptosis or proliferation prior to e21.5 pups were exposed to paracetamol as before, but were dissected at e17.5 after only 3 days of *in utero* exposure.

Gross morphological examination upon dissection demonstrated control animals were significantly smaller than paracetamol pups (0.62 ± 0.03 vs 0.81 ± 0.01 , $p < 0.0001$, Figure 4.12A). However, when analysed on a litter mean basis this reduction in body mass is no longer significant ($p = 0.15$, Figure 4.12B). AGD or AGI were not examined at e17.5 as little variance is seen at this age and no change had been determined at e21.5. These data demonstrate there is no gross morphological difference between control or paracetamol exposed fetal female rats at e17.5.

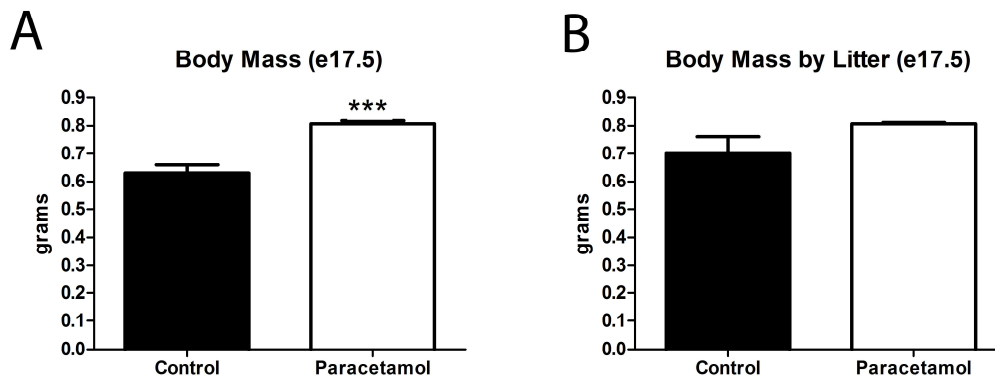


Figure 4.12 No difference in body mass of e17.5 fetal rats exposed to paracetamol

Body mass was recorded from e17.5 fetal female rats treated with 350mg/kg paracetamol (paracetamol) for 4 days of gestation or vehicle control (control). (A) Paracetamol exposed female were significantly larger than control animals when analysed as individuals. (B) When analysed as litter mean data, there was no significant difference seen between treatment groups (***) $p < 0.0001$.

4.3.8 No change in ovarian volume in e17.5 paracetamol exposed fetal rats

Ovarian volume was calculated as above for e21.5, to determine if a similar decrease in ovarian size could be detected at e17.5. A trend for increased ovarian size was seen in paracetamol exposed animals but this was not significant ($p=0.13$, Figure 4.13A). Analysis of ovarian volumes utilizing litter mean data also demonstrated no significant difference between control and paracetamol exposed pups ($p=0.36$, Figure 4.13B). These data demonstrate the significant change in ovarian volume seen at e21.5 is a result of action between e17.5 and e21.5 or requires the longer duration of exposure.

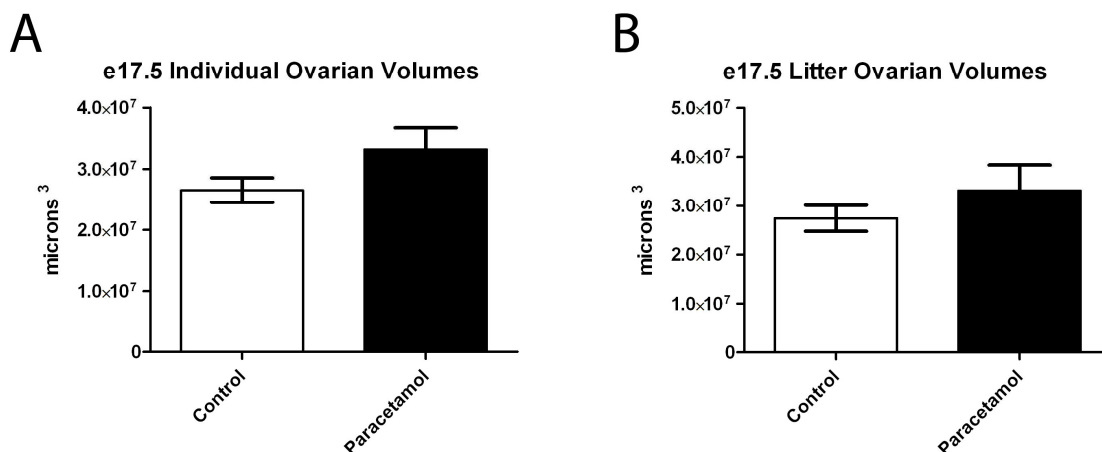


Figure 4.13 No change in fetal ovarian volume at e17.5

Fetal ovarian volumes were determined using stereological methods. (A) No change in ovarian volume was determined with paracetamol exposure (paracetamol) on an individual animal basis compared to control animals (control, $n=15$ control and treated animals). (B) Analysis using litter mean data also demonstrates no change with paracetamol treatment ($n=5$ litters for both treated and control).

4.3.9 No change in germ cell number with paracetamol exposure at e17.5

Although no change in ovarian volume was determined at e17.5, germ cell number per micron² was further evaluated at this age in order to determine any subtle changes in germ cell number. No change in germ cell density was determined on either the individual (p=0.84, Figure 4.14A) or on a litter mean basis (p=0.82, Figure 4.14B). This further demonstrates the significant change seen at e21.5 must be a result of effects between e17.5 and e21.5.

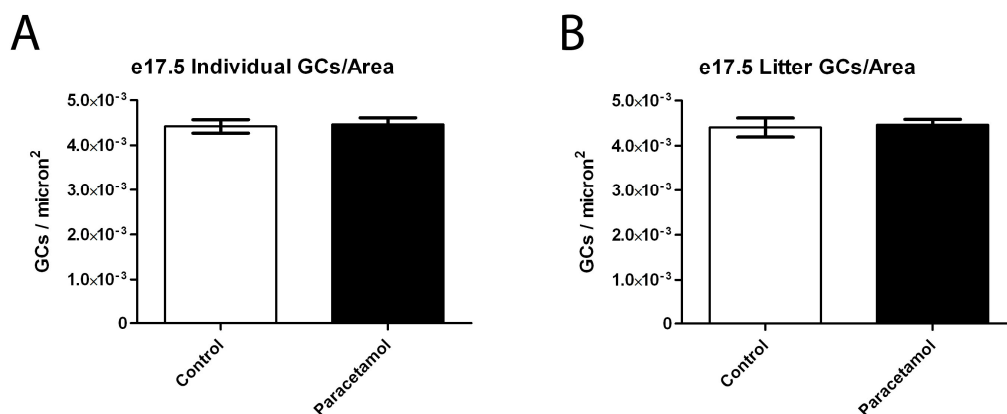


Figure 4.14 No change in germ cells per micron² with paracetamol exposure at e17.5

Germ cell number was determined using the nuclear germ cell marker VASA via stereological methods and adjusted for ovarian size. (A) Germ cell number in paracetamol treated pups (paracetamol) were not significantly different than that of control animals (control; n=15 for both groups). (B) No significant change was seen with paracetamol exposure when data was analysed using litter mean analysis (n=5).

4.3.10 No demonstration of altered apoptotic or proliferative rates at e17.5

No change in apoptosis or proliferation was seen at e21.5, which would indicate a cause for the demonstrated change in germ cell number. In order to determine if this change in germ cell number was a result of earlier change in cell turnover, both apoptosis and proliferation rates were examined in e17.5 ovaries. These rates were determined as previously described for e21.5, with CC3 or PHH3 positive cells per micron² adjusted for total number of germ cells per micron². No change was seen in apoptotic rate on either an individual ($p=0.87$, Figure 4.15A) or litter mean basis ($p=0.95$, Figure 4.15B). Additionally, no change was seen in proliferation rate on either an individual ($p=0.21$, Figure 4.16A) or litter mean basis ($p=0.40$, 4.16B). These results demonstrate there is no change in cell turnover at e17.5, suggesting either the change in cell turnover is acute between e17.5 and e21.5 or that the change in germ cell number may be due to loss via another mechanism.

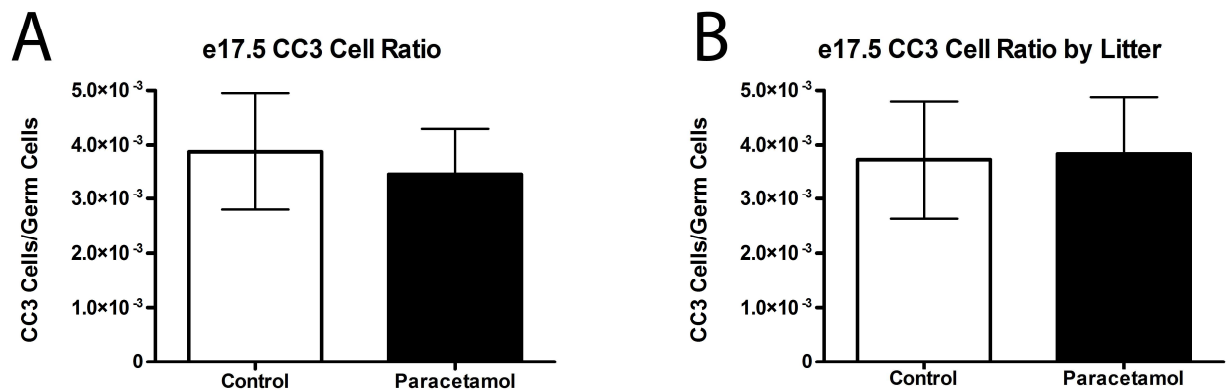


Figure 4.15 *Germ cell reduction in paracetamol ovaries not the result of increased apoptosis at 17.5.*

Rates of germ cell apoptosis were determined using the apoptotic marker cleaved caspase-3 (CC3) via stereological methods and adjusted for ovarian size. The number of CC3 germ cells per area was then adjusted for total germ cell number to demonstrate the proportion of CC3 positive germ cells per animal or litter. (A) No change was seen in ovarian apoptosis with fetal paracetamol exposure when examining changes in individual animals (n=15 animals per treatment). (B) This finding was confirmed using litter mean data (n=5 litters per treatment).

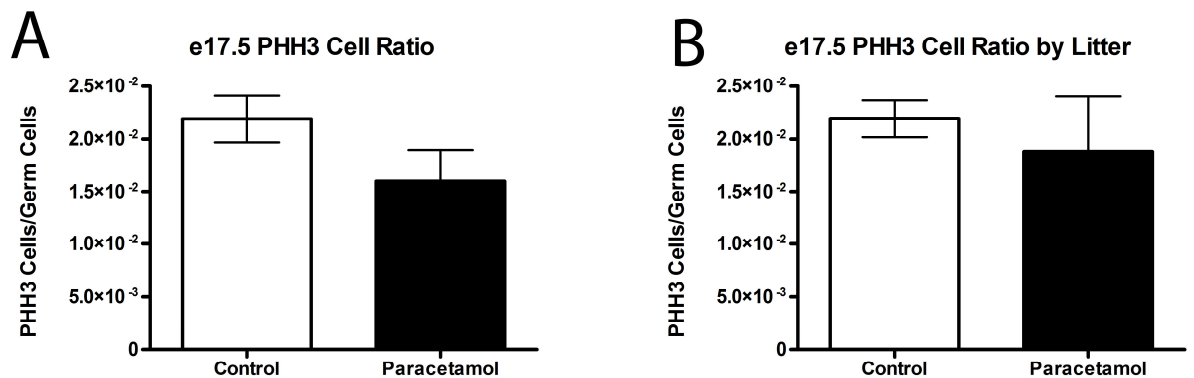


Figure 4.16 Germ cell reduction in paracetamol ovaries is not the result of decreased proliferation.

Proliferation rate was examined using the marker phospho-histone H3 (PHH3) via stereological methods and adjusted for ovarian size. The number of PHH3 germ cells per area was then adjusted for total germ cell number to demonstrate the proportion of PHH3 positive germ cells per animal or litter. (A) A trend was seen for less proliferation in individual paracetamol exposed ovaries when compared to control animals but was not significant (n=15 ovaries per treatment). (B) This trend was lost when analysed as litter mean data (n=5 litter per treatment).

4.3.11 Prostaglandin synthesis in the fetal rat ovary

In an effort to further elucidate possible causes of paracetamol exposure effects, further investigation of Cox and downstream prostaglandin signalling was investigated in the fetal rat ovary. The localisation of the Cox enzymes was identified in wild type e21.5 fetal rat ovaries. In addition, as Pge₂ was linked to germ cell survival in the human fetal ovary (as previously discussed in Chapter 3) (Bayne *et al*, 2009), Ptges, which is downstream of the Cox enzymes and responsible for Pge₂ specific synthesis, was also investigated.

Unlike the human, little Cox1 expression was seen in the fetal rat ovary (Figure 4.17A-B), although expression can be seen in blood cells. However, this expression is minimal, as shown by comparison with positive control tissue from the human endometrium (Figure 4.17C). Conversely, Cox2 expression was very similar to that seen in the human fetal ovary, displaying germ cell-specific localisation with variability between germ cells within the same germ cell nests (Figure 4.17D-F). Ptges expression was also similar to that seen in humans, with the majority of protein localised to the germ cells of the fetal ovary (Figure 4.17G-I). However, in the rat, unlike the human, expression is also seen in the pre-granulosa and somatic cells of the ovary. Distinct absence of Ptges expression can be seen in the capsule tissue surrounding the ovary, suggesting Ptges immunolocalisation in the fetal ovary is specific. These data demonstrate the primary site of Cox synthesis enzyme expression to be the germ cells in the fetal rat ovary, suggesting these are the targets of paracetamol action.

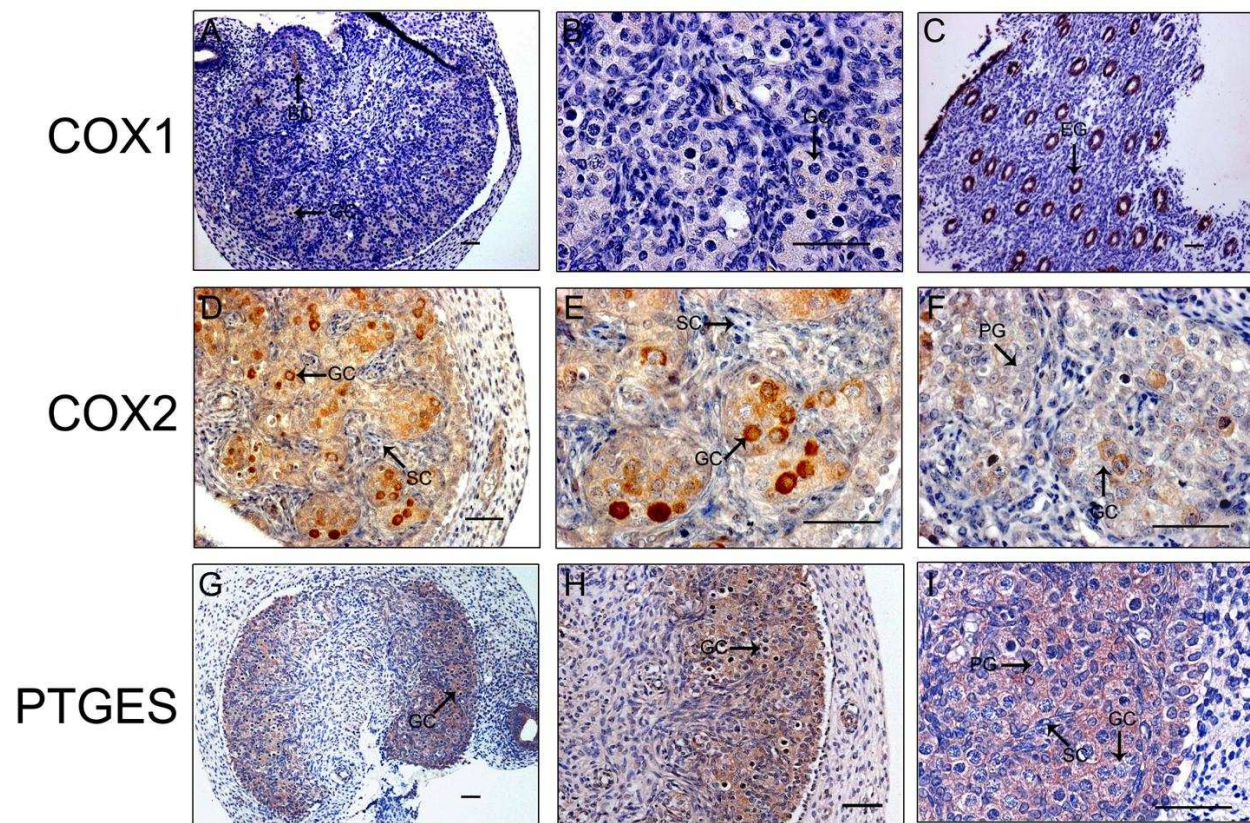


Figure 4.17 *Cox and Ptges expression in the wild type fetal rat ovary*

The Cox enzymes and Ptges were immunolocalised in the e21.5 fetal rat ovary. (A-B) Cox1 was mostly expressed in the blood cells (BC) of the fetal rat ovary with minimal expression in the germ cells (GC) compared to (C) glands in human endometrial tissue used as a positive control (EG). (D-F) Cox2 expression was exclusive to the germ cells of the rat fetal ovary with somatic cells (SC) and pre-granulosa cells (PG) remaining immune-negative. (G-I) Ptges was localized to all fetal ovarian cells in the rat, including GCs, SCs, and PGs. Scale bars equal 50 microns in all panels. Images are representative of staining performed on three separate e21.5 ovaries.

4.3.12 Pge₂ receptor expression in the fetal rat ovary

To determine the targets of the Cox product Pge₂, its four receptors (Ep1-4) were localised in the fetal rat ovary and compared to previous data from investigation in the human fetal ovary. Ep1 expression was similar to that of expression in the human ovary, with little expression seen outside of the blood cells within vessels, although slight expression was seen in some germ cells (Figure 4.18A-B). Ep2 expression was also similar to that seen in the human fetal ovary and was localised specifically to rat fetal germ cells (Figure 4.18C-D). Ep3 is also primarily expressed by fetal germ cells, although some Ep3 expression was seen in pre-granulosa cells, (Figure 4.18E-F). Ep4, unlike the other Pge₂ receptors, was localised to the nucleus of cells (Figure 4.18G-H), with primary localisation in somatic nuclei, but expression could also be seen in select germ and pre-granulosa cells. This expression was different to that seen in the human study, where EP4 expression was membranous. These results determine Pge₂ is capable of targeting various cell types in the rat fetal ovary, including the germ cells.

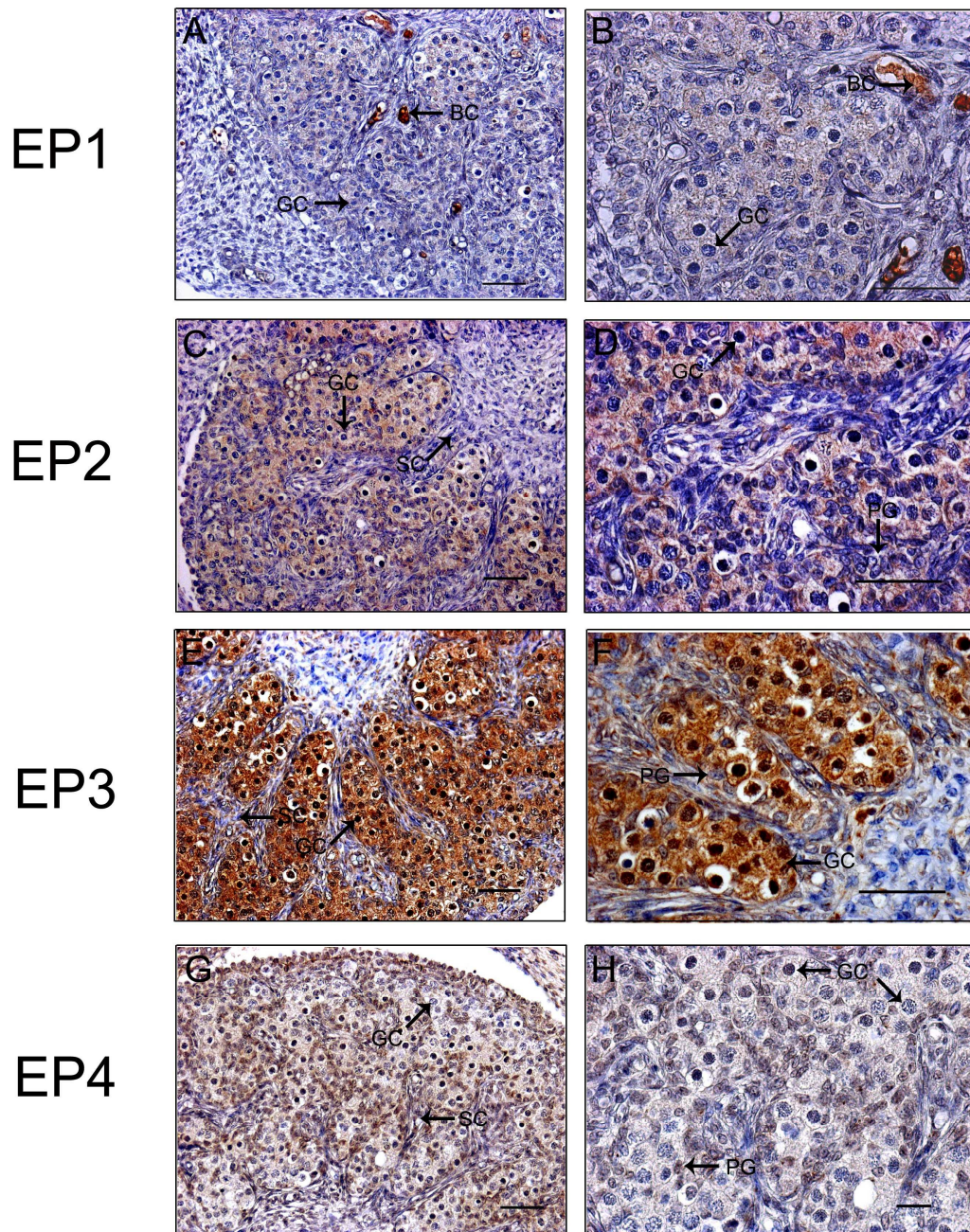


Figure 4.18 *Pge₂* receptor expression in the rat fetal ovary

Ep receptors were immunolocalised in the e21.5 fetal rat ovary to identify targets of *Pge₂* action. (A-B) Ep1 was expressed minimally by the germ cells (GC) but was predominately expressed by blood cells (BC) in the fetal rat ovary. (C-D) Ep2 expression was exclusive to the GC with no expression seen in somatic (SC) or pre-granulosa cells (PG). (E-F) Ep3 was localised to both the GC and PG of the germ cell nests in the rat fetal ovary, with negative SC streams. (G-H) Ep4 was localised to the nucleus of most cells in the ovary, predominately the SC, but also seen in the PG and some GC. Scale bars equal 50 microns. Images are representative of staining performed on three separate e21.5 ovaries.

4.4 Discussion

Germ cell development during fetal life is essential for adult fertility in the female. Disruption of early ovarian development can lead to premature ovarian insufficiency (POI) or infertility. Previous studies in the human fetal ovary identified PGE₂ as a possible regulator of this early germ cell development (outlined in Chapter 3 (Bayne *et al*, 2009)) but were unable to identify PGE₂ function due to the constraints of using human tissue. The rodent model of maternal paracetamol exposure utilised in this study, circumvents these issues, and provides further evidence for a role for Pge₂ in fetal ovarian development, as disruption of the Cox enzymes results in disruption of germ cell survival and maturation in female offspring. This disruption was quantified using the germ cell marker Tra-98, which is a nuclear marker similar to germ cell nuclear antigen (GCNA; (Bagheri-Fam *et al*, 2011)) which we were unable to obtain commercially. Tra-98 was utilised over other traditional germ cell markers because of its nuclear localisation, which allowed us to count both germ cell number as well as GCND using the same sections of ovary.

The reduction in germ cell number is likely to be the cause for the significantly smaller ovarian volumes observed, as no change was observed in overall body size of the treated pups. It was hypothesised this reduction in germ cell number might be the result of reduced proliferation or increased cell death. However, after quantifying markers for both proliferation and apoptosis, neither were found to be significantly altered in paracetamol treated ovaries compared to vehicle treated controls. It was further speculated that no change was seen in cell turnover at e21.5 as the alteration in germ cell number was a result of changes occurring earlier in gestation; however this theory was not supported by data collected from an earlier gestational group (e17.5). Additionally, e17.5 litters demonstrated no change in ovarian size or germ cell number with paracetamol exposure, suggesting that late gestational treatment (e17.5-e21.5) immediately before parturition in the rat is possibly a period susceptible to developmental disruption, and effects seen in e21.5 rats are due to change during this time. This hypothesis is supported by human meta-analysis data, indicated developmental effects of paracetamol and NSAIDs were heightened if exposure occurred during the second trimester in humans (Kristensen *et*

al, 2011), which is equivalent to late gestation in the rodent. However, it is also possible germ cells are lost via another unknown mechanism (eg autophagy).

It was further noted that remaining germ cells from paracetamol exposed pups at e21.5 had a reduced GCND, indicating the germ cells were developmentally delayed compared to control germ cells. However, the paracetamol treated germ cells did span the same diameters as compared to control germ cells ruling out complete arrest or specific loss of a subset of germ cells, but diameter was less synchronous in paracetamol exposed pups. These data indicated Cox products may play a role not only in germ cell survival but also maturation and possibly synchronicity. In further support of this theory, although not significant, both proliferation and apoptosis were heightened in paracetamol exposed germ cells at e21.5. These changes in cell turnover are only possible in pre-meiotic germ cells thus further suggesting the paracetamol exposed germ cells are developmentally delayed.

Based upon data collected from the human fetal ovary, it is postulated that inhibition of Pge₂ synthesis is likely to be at least one of the factors underpinning the germ cell effects seen with paracetamol exposure. To demonstrate Pge₂ is capable of targeting the germ cells in the fetal rat ovary, the Cox enzymes; Pge₂ specific enzyme, Ptges; and the Pge₂ receptors were immunolocalised in the wild-type rat fetal ovary. It is unlikely Cox1 plays a role in fetal ovarian development, as it was weakly expressed and is not greatly affected by paracetamol action (Hinz *et al*, 2008). In contrast, Cox2 was highly expressed in the germ cells of the rat fetal ovary, with variable expression between germ cells. This intense expression of Cox2 in specific germ cells may account for the partial loss of germ cells seen with paracetamol exposure, rather than a complete loss. Additionally, the Pge₂ specific synthesis enzyme Ptges is also expressed in germ cells; however, unlike in the human Ptges is also expressed in stromal and pre-granulosa cells of the rat fetal ovary. These results demonstrate that paracetamol is most likely to specifically affect Cox2 in the germ cells in the fetal ovary.

Secreted Pge₂ can then signal via one of the four Ep receptors, which were found to have specific, diverging expression patterns in the rat fetal ovary, as in the human. Expression of Ep1-3 was similar to that of the human fetal ovary. Conversely, Ep4 expression was not similar to that seen in the human, with primary localisation seen in somatic cell streams with variable expression in germ and pre-granulosal cells, although all expression was nuclear in the rat, unlike the membranous expression expected from a classical GPCR. This staining is not seen in negative control tissue, and likely to be specific. Both EP4 and EP2 have been reported to translocate intracellularly in some instances to act as transcriptional activators rather than membrane bound receptors, allowing development of a positive feedback loop (Figure 4.19) (Tjandrawinata & Hughes-Fulford, 1997; Inoue *et al*, 2000; Faour *et al*, 2008; Steinert *et al*, 2009). It is possible this localisation indicates Ep4 is acting directly to regulate transcription and in turn, increase Cox2 expression and Pge₂ synthesis. In support of this theory, Ep4 is only selectively expressed in the nuclei of a subset of germ cells as is heightened expression of Cox2. Although further evidence is needed for this mechanism, these results determine direct regulation of fetal germ cells in the rat ovary by Pge₂ is likely via Ep2, 3, or 4, with possible paracrine action mediated through Ep3 or 4, as Ep1 is minimally expressed. Although these data do not provide evidence for Pge₂ inhibition as the sole mediating factor affecting germ cells in paracetamol treated ovaries, they do provide further support for the role of Pge₂ during early fetal ovarian development.

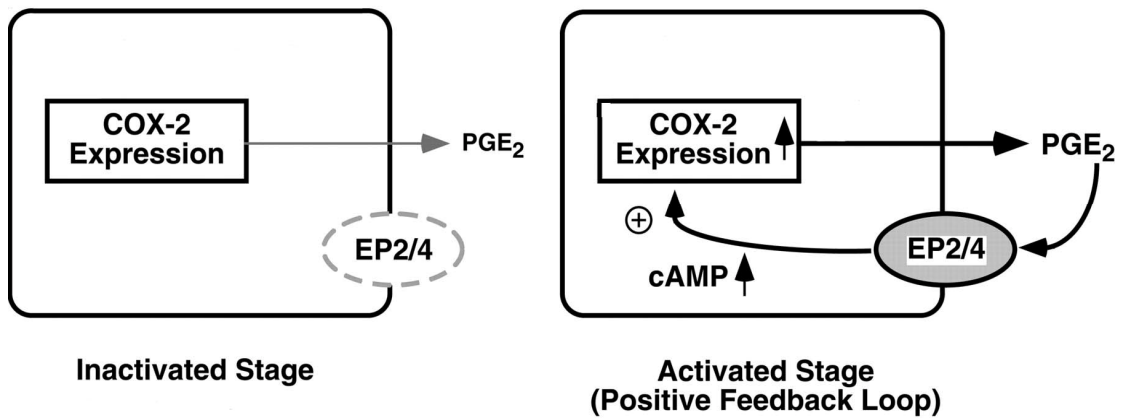


Figure 4.19 Positive feedback loop exerted via EP2/4 receptors during PGE₂ signalling.

Positive feedback loop mechanism utilized by PGE₂ via the two GPCRs EP2 and EP4. When inactivated, the cell expresses COX2 which in turn promotes secretion of PGE₂ and signaling via membrane bound GPCRs on neighboring cells. In an activated stage, the PGE₂ signals back to the cell via EP2 or 4 which then translocate inside the cell to promote sustained expression of the precursor enzyme COX2 via cAMP signaling maintaining a positive feedback system. Abbreviations: cAMP, cyclic AMP; COX2, cyclooxygenase-2; EP2/4, prostaglandin E receptor 2/4GPCR, g-coupled protein receptor; PGE₂, prostaglandin E2. Figure adapted from (Inoue *et al*, 2000).

Alternative factors possibly affected by paracetamol exposure have been suggested, including anti-androgenic signalling, as suggested in the previous studies of paracetamol exposure in male offspring (Gupta & Goldman, 1986; Gupta, 1989; Kristensen *et al*, 2011). Although no change in AGD/AGI was observed in the female pups of this study, there remains to be evidence this measure is indicative of steroid signalling in female offspring. However, male counterparts did show a significant fall in inter-testicular testosterone, as well as a reduction in AGD/AGI, consistent with a reduction in fetal androgens (data not shown). This fall in testosterone was also paired with a reduction in male germ cell number and an evident delay in maturation of germ cells with paracetamol exposure, similar to that seen in the female pups. Studies in mouse, rat and human fetal ovaries have demonstrated enzymes and receptors necessary for steroid synthesis and signalling are expressed during early ovarian development preceding primordial follicle formation suggesting these pathways are active

(Weniger, 1993; Chen *et al.*, 2007b; Chen *et al.*, 2009; Fowler *et al.*, 2011). Further, Chen *et al.* demonstrated progesterone/estrogenic signalling is capable of regulating both germ cell nest breakdown and primordial follicle formation in the mouse (Chen *et al.*, 2007b). Thus altered steroid signalling may lead to early nest breakdown which would result in germ cell loss. However, there is little evidence for this as a possible mechanism as estrogen receptor null mice do not display any disruption of fetal ovarian development and establish a normal cohort of primordial follicles (Dupont *et al.*, 2000; Couse *et al.*, 2001). In addition, a progesterone receptor-null model was also examined and deemed to develop phenotypically normal ovaries (Lydon *et al.*, 1995). Alternatively, as in the male, testosterone might be the steroid altered by COX inhibition. Although little is known about testosterone's role in the fetal ovary, it is known that the receptor by which it signals, androgen receptor (AR), is important for ovarian function. This was determined in an AR knockout (ARKO) mouse model, which demonstrated premature ovarian insufficiency at 8 weeks of age, despite what was deemed a normal compliment of follicles after birth (Shiina *et al.*, 2006). It is clear from these results, testosterone does play a role in ovarian biology; however lack of functional data regarding its role during fetal ovarian development obscures further postulation of what functions might be disrupted by COX inhibition at this time.

Another factor to be considered is maternal metabolism, with a possible metabolite of paracetamol or a change in liver response due to the additional metabolic effects of paracetamol resulting in downstream fetal effects. Paracetamol is almost entirely metabolised into other substances before being excreted (~98%), only one of these resulting metabolites, accounting for ~4% of total paracetamol metabolism, is known to be potentially toxic (Prescott, 1980). This toxic metabolite is the highly reactive alkylating agent, benzoquinoneimine, which in normal rodent and human metabolism is swiftly inactivated by conjugation with glutathione in the liver (Prescott, 1980). However, in cases of paracetamol toxicity, the amount of benzoquinonemine exceeds the glutathione produced, allowing for the excess metabolite to bind to liver cells causing acute necrosis (Mitchell *et al.*, 1977). As no liver necrosis was observed in the dams, it is thought this is not the cause of the fetal effects of paracetamol;

however, further studies investigating rate of paracetamol clearance would demonstrate if even minute paracetamol toxicity is occurring, as rate of clearance is slowed in animals experiencing paracetamol poisoning (Prescott & Wright, 1973).

Additionally, paracetamol's direct mechanism of action remains unknown, making it possible for an alternative unidentified signalling pathway (not a result of Cox inhibition) to be the cause of the developmental disruptions. In order to rule out these two possibilities, *in vitro* culture of fetal rat ovaries using the same gestational ages (e13.5-e20.5) were attempted with treatment of paracetamol and indomethacin (a COX specific inhibitor with known mechanism) (data not shown). These cultures would provide evidence for an ovarian specific effect outwith maternal and fetal metabolism; and if effects seen with indomethacin mimicked that of paracetamol, that effects were a result of Cox inhibition. However, these cultures were unsuccessful, as tissue recovered was highly distorted. This distortion was likely due to being harvested close to sex determination and/or the length of culture, as tubular structures were identified in both sexes as well as a lack of proliferating germ cells. An additional attempt was made using gonads from slightly later in gestation (e15.5) with culture treatment for a shorter time period but this too resulted in widespread apoptosis in all treatment groups.

In conclusion, although further study is required to determine if Pge₂ disruption is the cause of germ cell loss and delay seen in e21.5 paracetamol exposed fetal ovaries, this study has demonstrated there is an effect on fetal ovarian development with the use of the common analgesic paracetamol which inhibits the Cox enzymes upstream of Pge₂ synthesis. Additionally, components necessary for Pge₂ signalling are present in the fetal rat ovary with most components expressed in a similar localisation to that of the human fetal ovary, in which Pge₂ signalling has been demonstrated to regulate factors involved in proliferation and survival. Absence of this regulation might result in germ cell loss or developmental disruption, the two main effects seen in paracetamol exposed fetal ovaries.

Overall, these data demonstrate fetal exposure to paracetamol affects fetal germ cell number, and may thereby affect the number of primordial follicles formed. This would further affect the number of follicles available for ovulation and thus may lead

to POI in fetuses exposed to sustained paracetamol during *in utero* development. Further, investigation is necessary to determine if there are effects seen postnatally in paracetamol exposed female (and male) pups. As paracetamol is one of the most common drugs to take during pregnancy in the human, this may have relevant clinical implications (Werler *et al*, 2005). Additionally, incidence of POI, most of which is unexplained, remains high, this may further the understanding of mechanisms predisposing women to early follicle loss (Coulam, 1986).

Chapter 5

IL6-type cytokines in the human fetal ovary

Chapter 5. IL6-type cytokines in the human fetal ovary

5.1 Introduction

The IL6-type cytokines, which include IL6, leukaemia inhibitory factor (LIF), oncostatin M (OSM), and ciliary neurotrophic factor (CNTF), are well characterized regulators of the immune response. IL6-type cytokines also play key roles in the regulation of cell proliferation, differentiation and survival during embryonic development (Heinrich *et al*, 1998). LIF has a well characterized role in the maintenance of pluripotency in mouse embryonic stem (ES) cells (Williams *et al*, 1988), and consistent with this can (in the presence of basic fibroblast growth factor (bFGF) and KL) promote the conversion of PGCs into pluripotent ES cell-like Embryonic Germ (EG) cells (Matsui *et al*, 1991; Resnick *et al*, 1992). LIF can also increase isolated mouse PGC numbers *in vitro* (Pesce *et al*, 1993b; Cheng *et al*, 1994), as does OSM, CNTF, or IL6 (when cultured in the presence of the soluble isoform of its receptor) (Resnick *et al*, 1992; Cheng *et al*, 1994; Koshimizu *et al*, 1996). It has been suggested this results from an anti-apoptotic action of IL6-type cytokines on germ cells, rather than through the promotion of proliferation (Pesce *et al*, 1993a). LIF (and IL6 in conjunction with soluble receptor) also inhibits the spontaneous entry of mouse primordial germ cells into meiosis (Chuma & Nakatsuji, 2001), and has been shown to promote the primordial to primary follicle transition *in vitro* (Nilsson *et al*, 2002).

The IL6-type cytokines signal by forming dimers or trimers of various receptor components including two shared components glycoprotein-130 (gp130) and LIF receptor (LIFR) (reviewed in Heinrich *et al*, 1998 and depicted in Figure 5.1). LIF and OSM signal via heterodimeric complexes of gp130 in combination with LIFR, and additionally, OSM can signal through an alternative receptor complex consisting of gp130 and an OSM specific receptor (OSMR). CNTF utilizes a specific heterotrimeric complex of gp130, LIFR and a specific α -receptor subunit CNTF receptor (CNTFR). IL6 also signals via a trimeric complex consisting of a gp130 homodimer combined with its specific α -receptor subunit IL6 receptor (IL6R). The

α -receptor subunits (IL6R and CNTFR), although necessary for formation of specific receptor complexes, do not themselves transduce signal, whereas gp130, LIFR, and OSMR trigger phosphorylation of Janus (JAK) Kinases, in order to activate the Jak/STAT signalling cascade (Heinrich *et al*, 1998). As a direct result of utilizing similar receptor complexes, the IL6-type cytokines have overlapping biological activity (Taga & Kishimoto, 1997), and this biological redundancy has hindered efforts to elucidate the function of specific ligands. Thus *in vivo* results from genetically engineered animal models with target disruptions of IL6-type ligands and receptors have not recapitulated the effects of IL6-type cytokines on germ cells *in vitro* (Stewart *et al*, 1992; Escary *et al*, 1993; Ware *et al*, 1995; Yoshida *et al*, 1996; Molyneaux *et al*, 2003a).

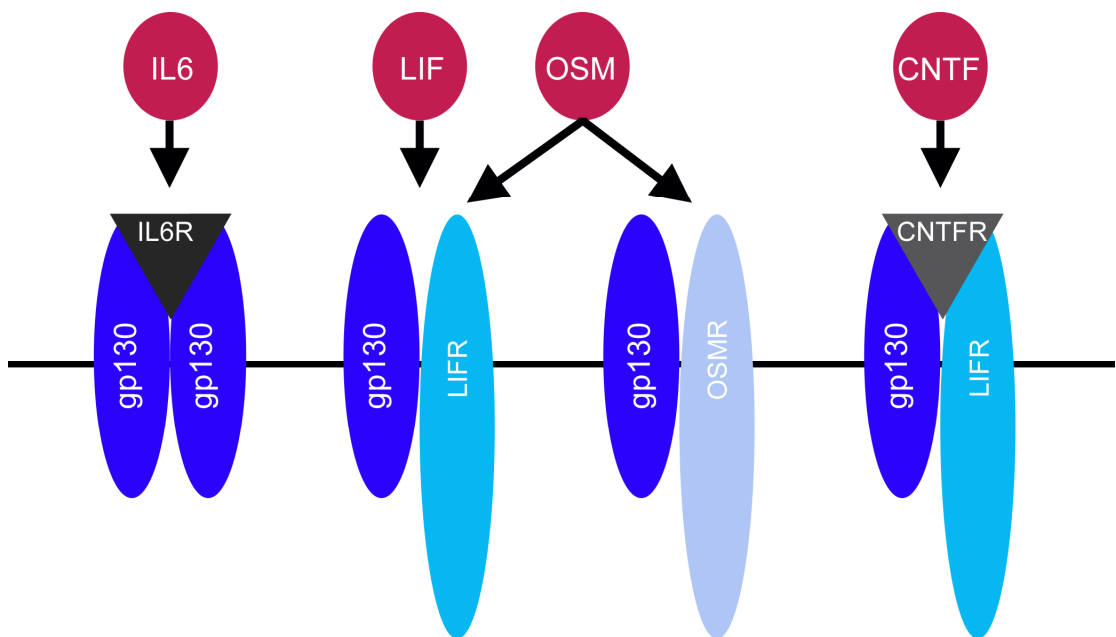


Figure 5.1 *IL6-type cytokines signal via receptor complexes.*

IL6-type cytokine complexes are made of shared signal transducing components (light blue) and α -receptor subunits (black and grey) that are necessary for specific ligand binding. The OSM ligand can bind a receptor complex consisting of gp130 homodimerised to LIFR or OSMR (reviewed in Heinrich *et al*, 1998).

Transcripts encoding LIF, gp130, and LIFR are expressed in the late fetal and adult human, and receptors are localized to oocytes (Abir *et al*, 2004). However, the expression of these factors during the key developmental window encompassing PGC proliferation, the initiation of meiosis and the formation of primordial follicles in the human fetal ovary has not been previously reported. We therefore examined the expression of *LIF*, *IL6*, *OSM*, and *CNTF*, as well as their receptor components in the human fetal ovary across increasing gestation from 8 to 20 weeks. We also investigated the expression and localization of gp130 and LIFR proteins to determine the cellular target(s) of IL6-type signalling, as a basis for understanding the roles that these cytokines might play *in vivo* in the human.

5.2 Materials and Methods

Tissue collection and dissection

Human fetal tissue used in the following experiments was obtained and dissected as described previously (Section 2.1), with subsequent SRY genotyping to determine sex of first trimester specimens (Section 2.3).

RNA extraction and cDNA synthesis

Sample tissue was then processed to extract RNA and subsequently synthesis cDNA for genomic analysis as previously discussed (Section 2.4).

Quantitative RT-PCR

In order to determine if mRNA transcripts encoding IL6-type cytokine ligands (IL6, LIF, OSM and CNTF) and receptors (gp130, IL6R, LIFR, OSMR) varied across gestation, qRT-PCR was performed using the ABI 7500Fast system and both Sybr Green and Taqman analysis as described in Section 2.5.

Statistical Analysis

Quantitative RT-PCR data were analysed with GraphPad Prism version 4 statistical software (GraphPad Software Inc). Gestational comparison data were analysed using one-way ANOVA, data were then either analysed as described or log-transformed for further analysis. Log-transformation was performed in instances where data sets did not fit a Gaussian distribution. The Kolmogorov-Smirnov normality test was used for this purpose.

Data were then analysed utilising the Newman-Keuls Multiple Comparison post-test to determine significant changes between gestational values. This post-test was chosen as has more strength than a Tukey post-test and the risk of type I error does not occur with only three groups (as in our study). Some data was also analysed using a post-test for linear trend, this test was performed when data looked to be in a natural order (increasing or decreasing across gestation).

Immunohistochemistry

In order to determine the cell-specific sites of IL6-type cytokine signalling, the common receptor components gp130 and LIFR were immunolocalised across gestation as outlined in Section 2.8.

5.3 Results

5.3.1 Genes encoding IL6 ligands are developmentally-regulated

To determine presence and pattern of expression of transcripts encoding IL6-type cytokines during human fetal ovarian development, we performed qRT-PCR for *IL6*, *LIF*, *OSM*, and *CNTF* across a range of gestations. Ovarian specimens were grouped into three gestational stages to broadly reflect the key developmental events of early to mid-gestation ovarian development, namely; the proliferation of undifferentiated PGCs (8-11 weeks gestation; first trimester), the formation of germ cell nests and entry of the first germ cells into meiosis (13-16 weeks; early second trimester) and on-going meiotic entry and the onset of primordial follicle formation (17-20 weeks; late second trimester).

Transcripts encoding all four ligands investigated were detected in the human fetal ovary. Expression of transcripts encoding IL6 increased by a modest but significant amount between first and early second trimester ($1.6 \pm 0.3 \times 10^{-4}$ vs $3.0 \pm 0.4 \times 10^{-4}$ relative to expression of the housekeeping gene *GAPDH*, $p=0.03$, $n=5-6$ per group) weeks gestation, but declined subsequently, such that expression at late second trimester ($1.9 \pm 0.2 \times 10^{-4}$ relative to *GAPDH*) was significantly lower than early second trimester (but not significantly different from first trimester ($p=0.04$)) (Figure 5.2A). *OSM* expression increased significantly with increasing gestation, starting at a borderline detectible level at first trimester ($2.3 \pm 0.5 \times 10^{-5}$ relative to *GAPDH*), increasing at early second trimester ($9.2 \pm 3.1 \times 10^{-5}$ relative to *GAPDH*), and again at late second trimester ($1.9 \pm 0.8 \times 10^{-4}$ relative to *GAPDH*, linear trend $p=0.04$, Figure 5.2B). In contrast, the expression of *LIF* and *CNTF* did not change significantly across the gestational range examined ($p=0.69$ and 0.17 respectively, Figure 5.2C and D). Transcript levels for *CNTF* were variable. These data reveal transcripts encoding IL6 and OSM are developmentally-regulated but expression of *LIF* and *CNTF* is not.

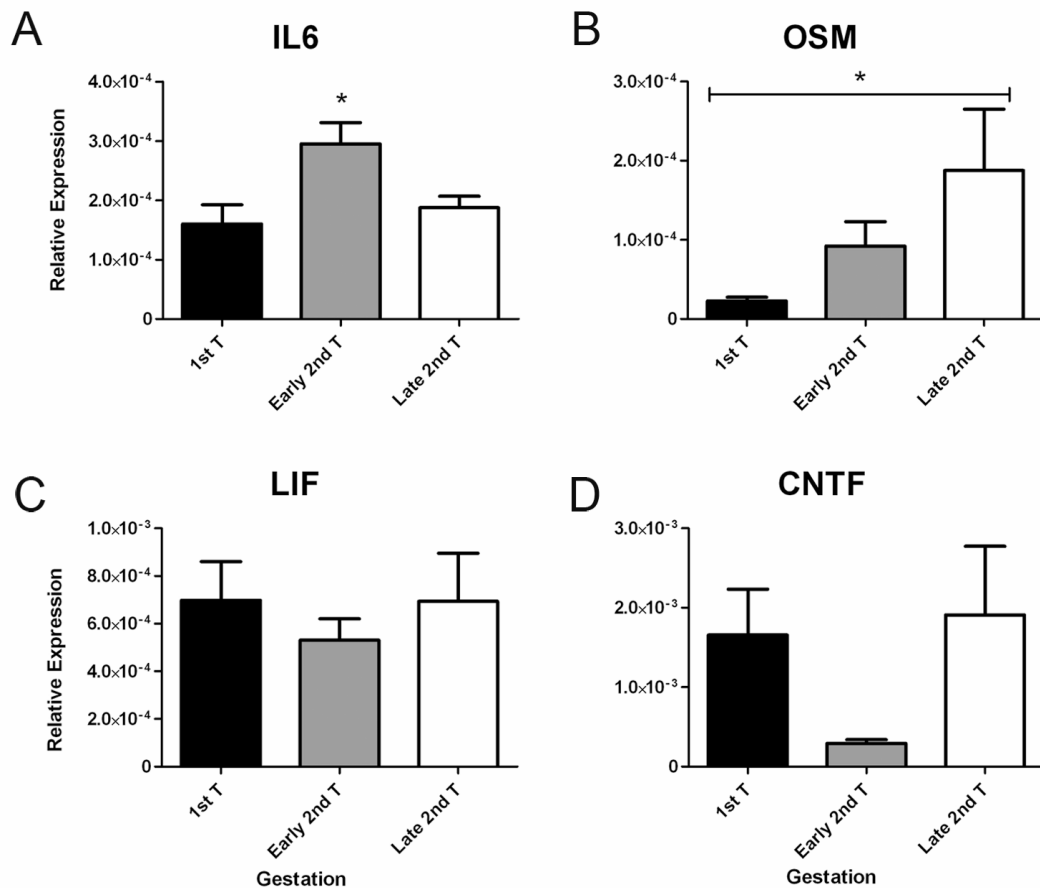


Figure 5.2 *Genes encoding the IL6-type ligands are developmentally regulated in the human fetal ovary.*

Genes encoding the IL6-type ligands are developmentally regulated in the human fetal ovary. Expression of the four ligands (IL6, LIF, OSM and CNTF) was analysed by qRT-PCR across gestation and split into age groups concordant with gestational events; PGC proliferation in 8-11 weeks (1st trimester), meiosis and germ cell nest formation in 13-16 weeks (early 2nd trimester), and primordial follicle formation in 17-20 weeks (late 2nd trimester); n= 4-6 samples for each gestation). (A) Expression of *IL6* increased between 1st and early 2nd trimester, and was subsequently decreased at late 2nd trimester (*= $p < 0.05$). (B) *LIF* expression did not change during early ovarian development. (C) Transcript levels for OSM are significantly up-regulated across gestation (*= $p < 0.05$, determined by test for linear trend). (D) *CNTF* expression was variable but no significant change across gestation was determined. Values denote mean \pm standard error of the mean relative to the housekeeping gene *GAPDH*.

5.3.2 Expression of transcripts encoding IL6-type cytokine receptors are developmentally-regulated

We next examined the expression of transcripts encoding the IL6-type cytokine receptors gp130, LIFR, OSMR, and IL6R across the gestational range outlined above (n=5-6 per gestational group). Expression of transcripts encoding both of the common signalling receptor components (gp130 and LIFR) increased between first and second trimester. Messenger RNA expression of gp130 was significantly greater at early second trimester ($2.1 \pm 0.3 \times 10^{-2}$ relative to *GAPDH*, $p=0.02$) and late second trimester ($2.1 \pm 0.3 \times 10^{-2}$ relative to *GAPDH*, $p=0.05$, Figure 5.3A) than at first trimester ($1.0 \pm 0.1 \times 10^{-2}$ relative to *GAPDH*). The mRNA expression of LIFR displayed a similar pattern, with expression at first trimester ($1.3 \pm 0.2 \times 10^{-2}$ relative to *GAPDH*) significantly lower than that at both early ($5.9 \pm 1.2 \times 10^{-2}$ relative to *GAPDH*, $p=0.01$) and late second trimester ($7.4 \pm 1.6 \times 10^{-2}$ relative to *GAPDH*, $p=0.01$, Figure 5.3B). *IL6R*, which is required for the IL6 signalling complex, but does not actively signal itself, was higher at late second trimester ($8.8 \pm 0.9 \times 10^{-2}$ relative to *GAPDH*) compared to both first ($3.5 \pm 0.6 \times 10^{-2}$ relative to *GAPDH*, $p=0.002$) and early second trimester ($1.8 \pm 0.7 \times 10^{-2}$ relative to *GAPDH*, $p=0.0003$, Figure 5.3C). Expression of *OSMR*, which also conducts intracellular signalling, displayed a similar trend to that of transcripts encoding gp130 and LIFR (i.e. increasing with gestation) but showed no significant changes across the gestational range examined (Figure 5.3D). These data demonstrate the two common receptor components and the IL6 specific component increase with gestation.

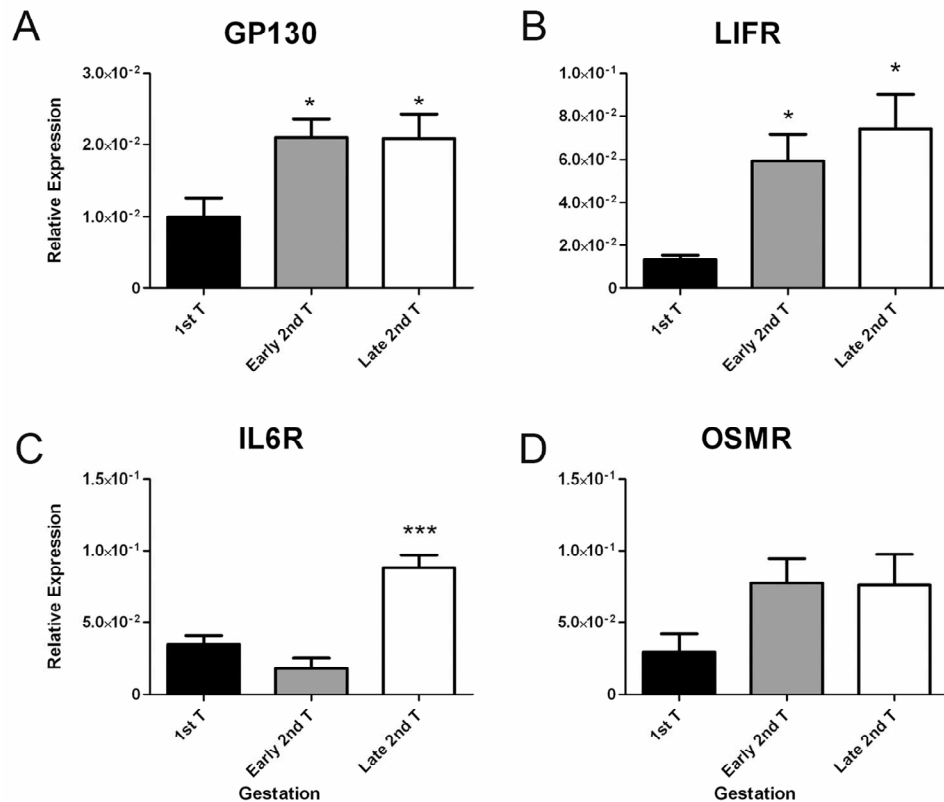


Figure 5.3 Expression of the common receptor components for the IL6-type cytokines increases with gestation in the human fetal ovary.

Expression of the common receptor components for the IL6-type cytokines increases with gestation in the human fetal ovary. Expression of receptor components necessary for IL6-type signalling was analysed by qRT-PCR across gestation. (A) Expression of *IL6ST* which encodes for gp130, was significantly higher in early and late 2nd trimester fetal ovaries than in 1st trimester samples (*= $p < 0.05$). (B) *LIFR* showed a similar pattern of expression, with a significant increase in transcript levels at 1st trimester compared to early and late 2nd trimester (*= $p < 0.05$). (C) *IL6R* was increased at late 2nd trimester compared to 1st and early 2nd trimester, concomitant with initiation of primordial follicle formation (**= $p < 0.001$). (D) Although sharing a similar trend to that of gp130 and *LIFR* expression, *OSMR* expression did not change across gestation. Values denote mean \pm standard error of the mean relative to the housekeeping gene *GAPDH*.

5.3.3 gp130 and LIFR are expressed exclusively by the germ cells in the human fetal ovary

To determine the cellular target(s) of IL6-type cytokine signalling in the human fetal ovary, we performed immunohistochemistry to detect the functional receptor components gp130 and LIFR across the developmental window outlined above. At 8 weeks gestation, gp130 expression was detected in germ cells, but staining was weak and sporadic and many germ cells displayed no staining (Figure 5.4A). In contrast, from 14 weeks gestation, expression was stronger and restricted to germ cells, with stromal cell streams and pre-granulosa cells not showing any expression (Figure 5.4B and C), a pattern maintained in later gestations (Figure 5.4D and E). Staining was also detected in oocytes in primordial follicles at 20 weeks gestation (Figure 5.4E inset), revealing that germ cells continue to express gp130 following nest breakdown and follicle assembly.

The expression pattern of LIFR in the human fetal ovary was similar to that of gp130, with staining detected exclusively in germ cells from 8 weeks of gestation onwards (Figure 5.5A-D). Notably, germ cells displayed variability in the intensity of LIFR staining even within close proximity (Figure 5.5E). At 20 weeks gestation, oocytes within primordial follicles expressed LIFR (Figure 5.5E inset). The expression pattern of the two shared, functional signalling components indicates that IL6-type cytokines are able to signal to germ cells in the fetal ovary; indeed germ cells appear the sole cell type involved.

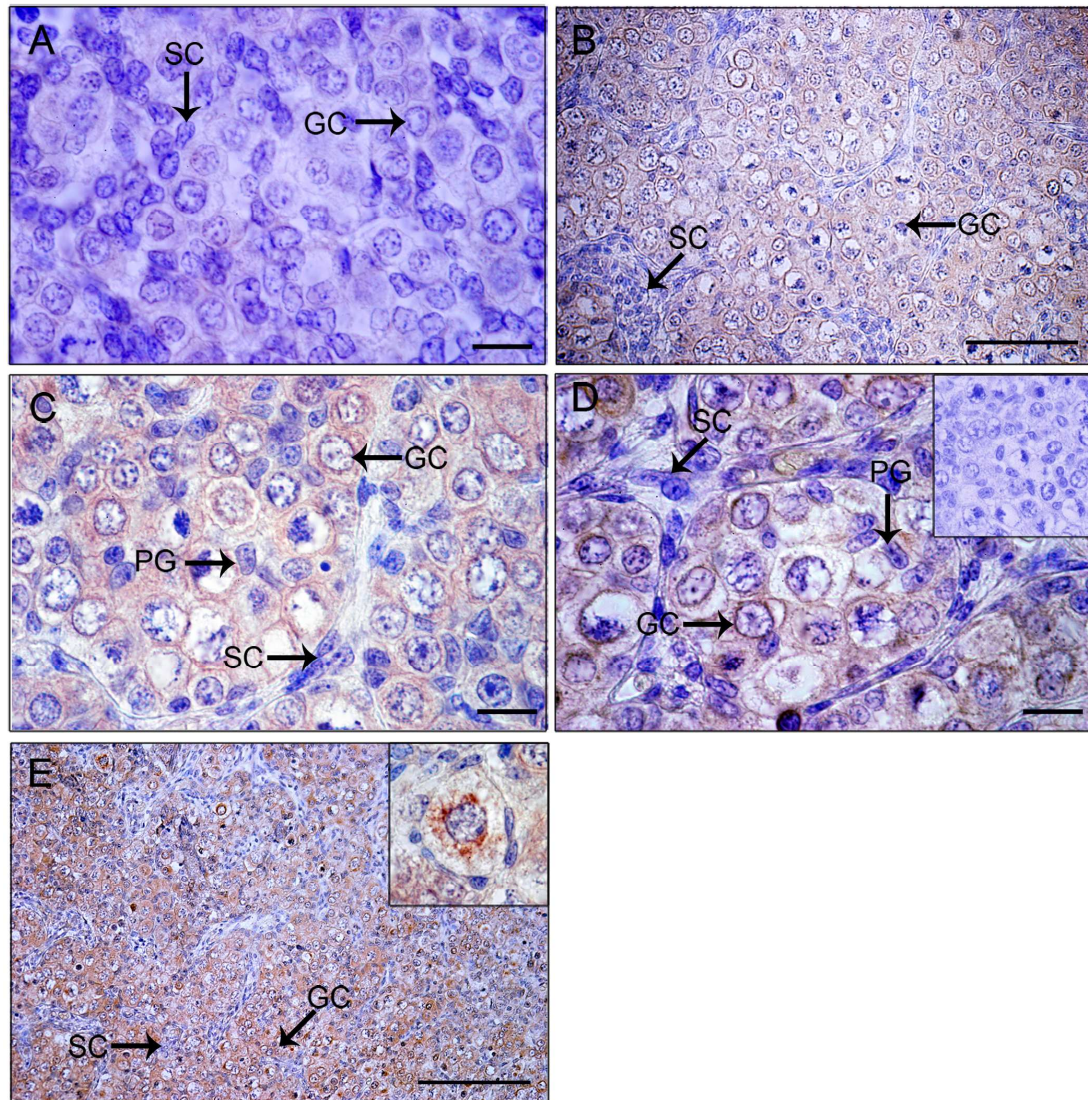


Figure 5.4 *Immunohistochemical detection of gp130 in the fetal ovary.*

Immunohistochemical detection of gp130 in the human fetal ovary across gestation. (A) At 8 weeks gestation, faint gp130 staining is detectable in some germ cells (GCs), but the majority show no expression. At 14 weeks (B and C) and 17 weeks (D), clear gp130 expression can be seen in the GC clusters, whilst stromal somatic cell streams (SC) and pre-granulosa cells (PG) remain immuno-negative. (D, Inset) Negative control sample, lacking primary antibody, is absent of any non-specific staining. (E) At 20 weeks gestation, gp130 staining is more distinct and with immuno-positive GCs (E Inset) including oocytes within primordial follicles. Scale bars equal 10 μm in (A) (C) and (D), 25 μm (B), and 50 μm in (E). Images are representative of staining performed on at least 2 specimens at roughly the same gestation.

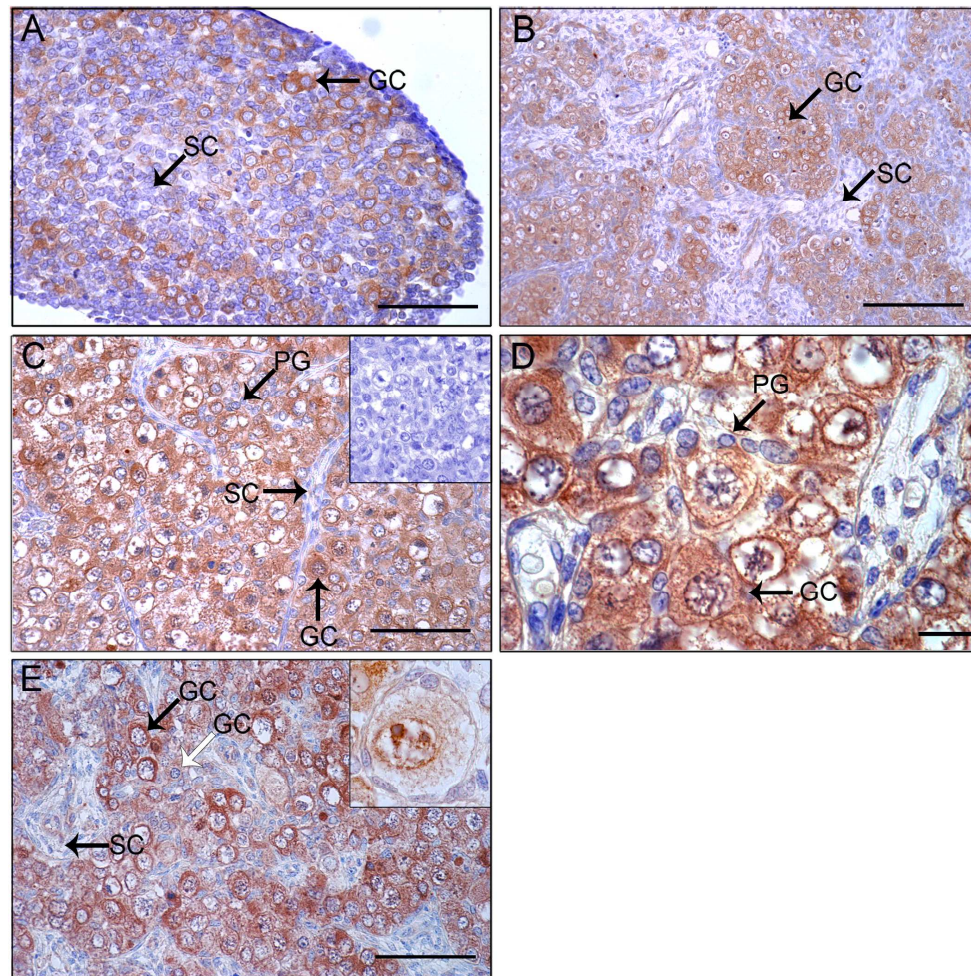


Figure 5.5 *Immunohistochemical detection of LIFR in the fetal ovary*

Immunohistochemical detection of LIFR, is expressed in the human fetal ovary. (A) At 8 weeks gestation, germ cell (GC)-specific staining for LIFR is detectable. (B) GC clusters at 14 (B) and 17 (C and D) weeks express LIFR, with no staining detected in stromal somatic cell streams (SC) and pre-granulosa cells (PG) interspersed within germ cell clusters. (C, Inset) No immunostaining was detected in the negative control, demonstrating antibody specificity. (E) LIFR receptor expression at 20 weeks was localized specifically to germ cells, but variations in the intensity of staining between neighbouring germ cells is apparent (white and black arrows denote germ cells with weak or strong LIFR expression respectively). (E, Inset) oocytes in primordial follicles also expressed LIFR. Scale bars equal 10 μm in D, 25 μm in (A) and (C), and 50 μm in (B) and (E). Images are representative of staining performed on at least 2 specimens at roughly the same gestation.

5.4 Discussion

Germ cell development and primordial follicle formation are vital to female fertility. Extensive *in vitro* studies have demonstrated roles for LIF and other IL6-type cytokines in the regulation of germ cell development (Matsui *et al*, 1991; Resnick *et al*, 1992; Cheng *et al*, 1994; Koshimizu *et al*, 1996; Chuma & Nakatsuji, 2001; Nilsson *et al*, 2001). However, little evidence has been provided regarding their potential roles during human fetal ovarian development. The data presented here confirm that all IL6-type cytokines previously demonstrated to regulate murine germ cell development *in vitro* (LIF, IL6, OSM, and CNTF) are expressed in the human fetal ovary, as are their common receptor components. Furthermore, the expression of the latter is confined to germ cells, revealing these cells to be the exclusive targets of IL6-type signalling in the human fetal ovary.

Expression of the genes encoding IL6-type signalling components was found to be developmentally-regulated, a finding consistent with the immunohistochemistry data also presented here. Unexpectedly, the finding that gp130 expression is low or undetectable in primordial germ cells in the first trimester human fetal ovary suggests that these cells have little or no capacity to receive and/or transduce IL6-type cytokine signals, and implies that, as in rodents (Molyneaux *et al*, 2003a), gp130 signalling activity is not required for the survival of human PGCs, or their maintenance in an undifferentiated state *in vivo*. The mRNA and protein levels of both gp130 and LIFR appear to be up-regulated in the early second trimester, however. This coincides with the entry of the first germ cells into meiosis (Gondos *et al*, 1986; Hibi *et al*, 1990), and indicates that IL6-type signalling may be important in the regulation of this critical event. As both LIF and IL6 are reported to inhibit the spontaneous initiation of meiosis of isolated mouse PGCs in culture (Chuma & Nakatsuji, 2001), it is possible that up-regulation of receptor expression functions to prevent precocious entry into meiosis, maintaining an immature cell population that can still undergo further proliferation. The absence of signalling in first trimester germ cells, and the lack of an apparent restriction of gp130 and LIFR expression to undifferentiated, pre-meiotic germ cells found at the periphery of the second trimester human fetal ovary (Anderson *et al*, 2007) casts doubt on this hypothesis.

More likely, IL6-type cytokines play a role in promoting the survival of differentiating/meiotic germ cells. Consistent with this, a modest anti-apoptotic effect was reported when LIF treatment was applied to germ cells in 3-day cultures of fetal mouse ovaries isolated from e13.5 mice (a development stage comparable to that of the early second trimester (13-16 weeks gestation) specimens reported here) (Morita *et al*, 1999). Of particular note is the striking variability in expression of LIFR in between germ cells, particularly at later gestations, similar to that we have reported recently for brain derived neurotrophic factor (BDNF) (Childs *et al*, 2010a). Given the anti-apoptotic role of IL6-type cytokines for germ cells at this developmental stage (Morita *et al*, 1999), it is possible that the germ cells expressing the highest level of LIFR may gain a selective survival advantage during the wave of oocyte death that accompanies nest breakdown and follicle formation. The increased expression of *IL6R* specifically in the late second trimester (as nest breakdown and primordial follicle formation commence) is also consistent with this hypothesis.

Expression patterns of the IL6-type ligand transcripts are more varied. No changes were detected in the expression of *LIF*, which is postulated to be involved in ovarian development (Nilsson *et al*, 2002), or *CNTF* across the gestational range examined (although the high variability in CNTF expression between specimens may mask such a change). Each of these ligands utilizes the same LIFR/gp130 receptor complex, however, only *OSM*, displays increasing expression with gestation similar to that of the two receptor components. The expression of both *IL6* and its specific receptor *IL6R* are also increased in second trimester, albeit at slightly different developmental stages. Together these data demonstrate that multiple components of the IL6-type cytokine signalling machinery are up-regulated in the second trimester human fetal ovary, suggesting potential roles for these factors in the later stages of germ cell development and primordial follicle formation.

Signalling by IL6-type cytokines has been reported to interact with other key signalling pathways that regulate mammalian ovarian development. OSM up-regulates the growth factor bFGF *in vitro* (Wijelath *et al*, 1997), which promotes primordial follicle formation (Nilsson *et al*, 2001). Similarly, KL expression is

regulated by LIF in rodent ovarian culture and is able to activate differentiation and promote survival in germ cells (Nilsson *et al*, 2002). It has thus been proposed that bFGF, KL, and the IL6-type cytokines have similar functions and work synergistically *in vivo* in the ovary (Kezele *et al*, 2002).

In addition to interactions with bFGF and KL, the IL6-type cytokines have been shown to interact in non-reproductive organs with cytokines known to regulate human ovarian development. LIF and BMP2, signalling through STAT3 and SMAD1 respectively, are known to act synergistically in promoting the differentiation of astrocytes from cultures of fetal neuronal precursor cells (Nakashima *et al*, 1999). We have recently reported increased expression of *BMP2* and *SMAD1* in the second trimester human fetal ovary, and identified germ cells to be the exclusive targets of BMP signalling in this tissue (Childs *et al*, 2010b); thus the apparatus for such a synergistic interaction between IL6-type cytokine and BMP signalling also exists in human fetal ovarian germ cells. LIF also acts synergistically with the neurotrophin BDNF to promote cell survival and proliferation in the developing rodent brain (Marzella *et al*, 1999). This is similar to the known role for BDNF in the rodent ovary (Spears *et al*, 2003; Paredes *et al*, 2004; Childs *et al*, 2010a).

To date, animal models have failed to determine *in vivo* roles for the IL6-type cytokines during ovarian development. Female *Lif*^{-/-} mice do manifest an infertility phenotype, but as a result of an implantation defect, rather than a disruption of germ cell development (Stewart *et al*, 1992; Escary *et al*, 1993). Successful ovulation of viable oocytes was confirmed, but quantity of follicles and long term fertility were not examined. Interestingly, LIF-deficient mice display a significant loss of stem cell populations in the spleen and bone marrow (Escary *et al*, 1993). To bypass the difficulty of IL6 ligand redundancy, mouse models with targeted disruptions of the genes encoding the gp130 and LIFR receptors have been generated, however, both models were either embryonically or early postnatally lethal (Ware *et al*, 1995; Yoshida *et al*, 1996), precluding a detailed analysis of their fertility. A mouse model in which gp130 is conditionally disrupted only in germ cells (gp130^{Δ/Δ}) has been also

been generated (Molyneaux *et al*, 2003a). Embryonic day (e) 13.5 gp130^{Δ/Δ} males showed significantly fewer PGCs, but mature males were fertile. Embryonic females had no difference in germ cell number; adult homozygous recessive females were infertile or produced small litters due to defects in ovulation or late oocyte maturation. In addition gp130^{Δ/Δ} females also had fewer primary follicles, but no difference in the number of primordial follicles.

Although this study does not explore the possible functions of the IL6-type cytokines, it does confirm they signal solely to the germ cells in the human fetal ovary at the gestations examined. Both the shared signalling components gp130 and LIFR, one or both of which are necessary for formation of all IL6-type signalling complexes, were immunohistochemically localized in germ cells and primordial follicles, suggesting any role the IL6-type cytokines would be via direct regulation of the germ cells. Previous reports regarding LIF localization in the human ovary suggest this is via juxtacrine signalling from pre-granulosa stromal cells or autocrine signalling from the germ cells themselves (Abir *et al*, 2004).

In conclusion, these data demonstrate that IL6-type cytokines are expressed in the human fetal ovary during germ cell development, and that germ cells are the sole target of IL6-type action in the fetal ovary. Additionally, transcripts for both ligands and receptors are developmentally regulated, increasing with gestation, suggesting that the IL6-type cytokines are important for *in vivo* development of the human ovary, predominantly regulating the transition of differentiating germ cells from the formation of germ cell nests, through the entry into meiosis and the formation of primordial follicles.

Chapter 6

Prokineticins in human fetal ovarian development

Chapter 6. Prokineticins in fetal ovarian development

6.1 Introduction

PROK1 and 2 are recently described proteins that are well characterised for their role in regulation of angiogenesis and inflammation ((Sales & Jabbour, 2003b; Ngan & Tam, 2008) as fully described in Chapter 1). The PROK ligands signal interchangeably via two GPCR receptors (PROKR1 and PROKR2; (Lin *et al*, 2002; Soga *et al*, 2002); Figure 6.1), and function similarly to vascular endothelial growth factor (VEGF) but are restricted to steroidogenic organs (adrenals, placenta, gonads, etc).

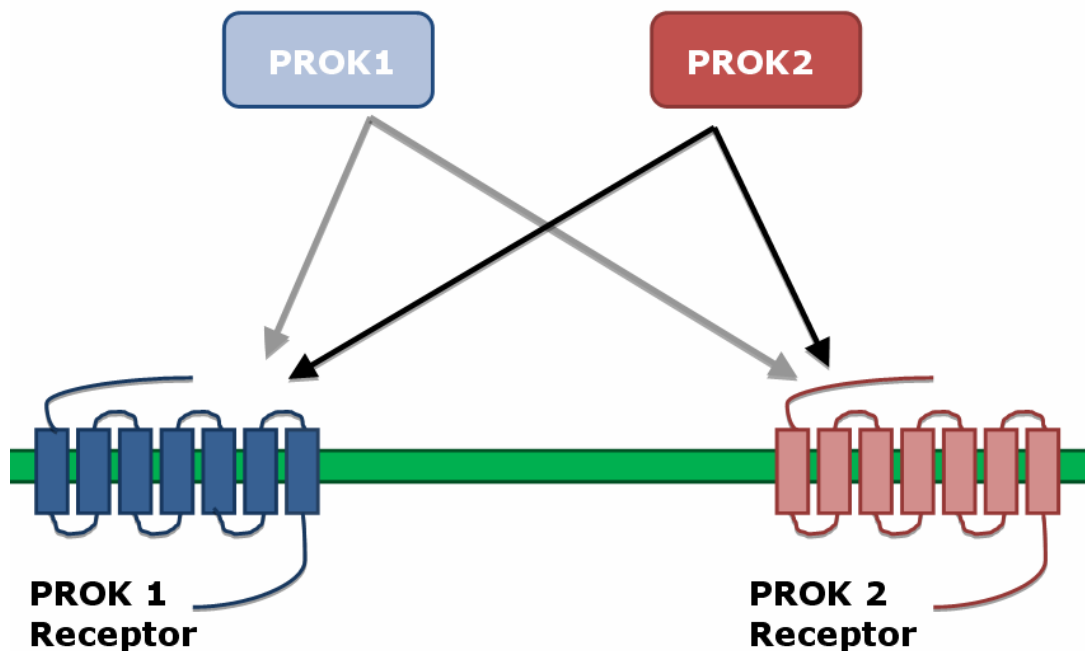


Figure 6.1 *PROK signaling components*

PROK1 and 2 signal via two shared g-coupled protein receptors (GPCRs); PROK receptor 1 (PROKR1) and 2 (PROKR2). Although the ligands are able to signal interchangeably, PROK2 has a higher affinity for both receptors compared to PROK1.

Angiogenesis is a key process in the cyclical activity of the normal adult ovary, as well as ovarian disorders including polycystic ovary syndrome (PCOS) and ovarian cancer (Bamberger & Perrett, 2002; Ferrara *et al*, 2003). For this reason the PROKs have been characterised in the adult ovary. In the human ovary, PROK1 mRNA is expressed highly in granulosa cells surrounding primordial and primary follicles, but expression declines sharply as the follicles mature to form secondary and antral follicles (Ferrara *et al*, 2003). PROK1 is also highly expressed in the remaining theca of atretic follicles and for this reason it has been suggested to function in remodeling and proliferation required for ovarian repair post-ovulation (Ferrara *et al*, 2003). In support of this hypothesis, studies in a bovine model have also suggested a role for PROK1 in proliferation and survival of cells within the corpus luteum (Kisliouk *et al*, 2003; Fraser *et al*, 2005).

Little is known about the other PROK signaling components in the ovary. It has been confirmed the two PROK receptors are expressed in the adult human ovary, however further localisation has not been performed (Lin *et al*, 2002; Soga *et al*, 2002). Additionally, PROK2 mRNA was not detectable in the human adult ovary in previous studies (Ferrara *et al*, 2003). Interestingly, homozygous deletion of the PROKR2 gene in a rodent model results in severe atrophy of the reproductive system including the ovary (Matsumoto *et al*, 2006; Pitteloud *et al*, 2007). However, it was determined that this was not due to direct action on the reproductive tract, rather via PROKR2's role in GnRH neuron development in the hypothalamus. Further, the *PROKR2*^{-/-} phenotype is distinctly similar to that of humans with Kallmann syndrome, and subsequent studies have identified PROK2 and PROKR2 mutations in several Kallmann patients (Dode *et al*, 2006).

Further characterisation studies of the PROKs and their role in the human fetal ovary during development have not been performed. However, two recent genetic array studies have examined the PROKs in the fetal ovary, with intriguing results. One transcriptome study suggested an increased role for PROK1 in the fetal mouse ovary compared to the fetal testis, as a result of increased transcript expression (Houmard *et al*, 2009). Another study detected developmentally-regulated expression of PROK2 in the fetal ovary (Fowler *et al*, 2009).

Outwith the ovary PROK1 has been demonstrated to regulate several factors known to be expressed and/or involved in ovarian development including LIF, the IL6-type ligand and COX2 the prostaglandin synthase (Evans *et al*, 2008; Evans *et al*, 2009). With this data in mind, it was hypothesised that PROKs might play a role in regulating these factors, as well as others to promote proliferation, differentiation and possibly angiogenesis during the development of the fetal ovary. In order to determine further PROK function, the two PROK ligands and their shared receptors were characterised across early gestation in the human fetal ovary. Functional investigation was then performed utilising the TCam-2 cell line, generated from adult (35 yrs) human testicular germ cell tumour (Mizuno *et al*, 1993).

TCam-2 cells expresses several pluripotency and developmental genes similarly to PGCs (Eckert *et al*, 2008; Young *et al*, 2011; Childs *et al*, unpublished) (Figure 6.2). These PGC markers include NANOG, OCT4, KIT, and VASA, which are classically associated with early germ cells (roughly comparable to the first trimester specimens utilised in this study (8-12 weeks)). The later germ cell marker DAZL, which is increasingly expressed in second trimester human fetal ovary (Anderson *et al*, 2007), is not detected in the TCam-2 cells at either the transcript or protein level supporting the comparability of these cells to PGCs. The TCam-2 line was utilised for further functional exploration of possible connections between PROK signalling and the other factors discussed in this thesis, as well as regulators known to be involved in germ cell proliferation and development.

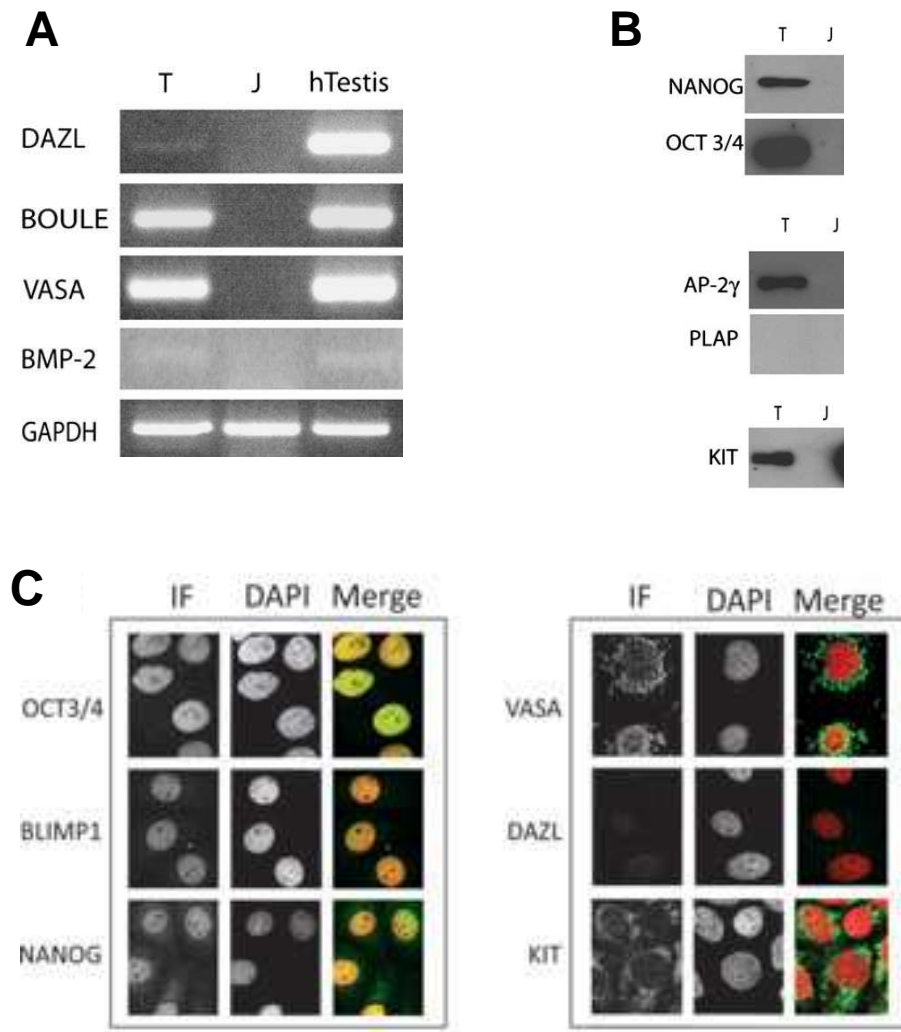


Figure 6.2 Previous characterization of the TCam-2 cell line

TCam-2 cells (T) express several pluripotent and early germ cell markers similar to primordial germ cells. (A-B) RT-PCR comparison of several factors with another seminoma line JKT-1 (J) and human testis (hTestis) demonstrate the TCam-2 expression profile closely mimics that of early germ cells. (C) TCam-2 cells also express pluripotent/germ cell markers at the protein level, as determined via immunofluorescence. Figure compiled (A) from (Childs *et al*, unpublished) (B) (Eckert *et al*, 2008) (C) (Young *et al*, 2011).

6.2 Materials and Methods

Tissue collection

Human fetal tissue used in the following experiments was obtained and dissected as described previously (Section 2.1), with subsequent SRY genotyping to determine sex of first trimester specimens (Section 2.3).

RNA extraction and cDNA synthesis

Sample tissue was then processed to extract RNA and subsequently synthesis cDNA for genomic analysis as previously discussed (Section 2.4).

Quantitative RT-PCR

In order to determine if mRNA transcripts encoding PROK signalling targets (PROK1, PROK2, PROKR1 and PROKR2) expression varied across gestation, qRT-PCR was performed using the ABI 7500Fast system and both Sybr Green and Taqman analysis as described in Section 2.5.

Quantitative RT-PCR analysis of PROKR1 transfected T-Cam2 cells was also performed using the ABI 7900HTFast system and Sybr Green analysis to determine gene expression changes in possible PROK targets (LIF, OSM, IL6, CNTF, PTGES, ID3, BDNF, MCL-1) and Taqman analysis was also performed for targets with primer/probe sequences (COX2), details of this protocol are also outlined in Section 2.5.

Immunohistochemistry

Human fetal ovarian samples were used to localise PROK ligands (PROK1 and 2) and receptors (PROKR1 and 2) to determine cell-specific sites of PROK synthesis and action. Protocols are described in detail in Section 2.8.

PROKR1 transfected T-Cam2 cell cultures

T-Cam2 cells stably transfected with the PROKR1 receptor were created as described in previously in Section and cultured in media as described in Section 2.13. Cells were cultured under standard procedures as described, and plated for treatment with vehicle control or 40nM PROK1 over a 24 hour time course, with cells harvested at 0, 2, 4, 6, 8, 12, and 24 hours after treatment to determine down-stream gene regulation. Cell cultures were collected in RLT buffer following culture and snap frozen for further RNA extraction and cDNA synthesis.

Statistical Analysis

Quantitative RT-PCR data were analysed with GraphPad Prism version 4 statistical software (GraphPad Software Inc). Gestational comparison data were analysed using one-way ANOVA, data were then either analysed as described or log-transformed for further analysis. Log-transformation was performed in instances where data sets did not fit a Gaussian distribution. The Kolmogorov-Smirnov normality test was used for this purpose.

Data were then analysed utilising the Newman-Keuls Multiple Comparison post-test to determine significant changes between gestational values. This post-test was chosen as has more strength than a Tukey post-test and the risk of type I error does not occur with only three groups (as in our study). Some data was also analysed using a post-test for linear trend, this test was performed when data looked to be in a natural order (increasing or decreasing across gestation).

Gene expression changes identified using qRT-PCR after PROK1 treatment of T-Cam2 cells were also analysed using GraphPad Prism as above. Data were analysed using paired t-tests comparing PROK1 treated cells to dH₂O treated cells (as the appropriate control).

6.3 Results

6.3.1 PROK signalling components are developmentally regulated in the human fetal ovary

To determine presence and pattern of expression of transcripts encoding PROK signalling components during human fetal ovarian development, qRT-PCR was performed for the two PROK ligands (*PROK1* and 2) and the two PROK receptors (*PROKR1* and 2) across a range of gestations. Ovarian specimens were grouped into three gestational stages, as in previous chapters to reflect broadly key developmental events; the proliferation of undifferentiated PGCs (8-11 weeks gestation; first trimester), the formation of germ cell nests and entry of the first germ cells into meiosis (13-16 weeks; early second trimester) and on-going meiotic entry and the onset of primordial follicle formation (17-20 weeks; late second trimester).

Transcripts encoding PROK ligands and receptors were expressed in the human fetal ovary across all gestations investigated. Expression of *PROK1* increased significantly in late second trimester compared to both first and early second trimester (2.0 ± 0.4 vs 0.4 ± 0.1 and $.9 \pm 0.3 \times 10^{-2}$ expression relative to the housekeeping gene *GAPDH*, $p=0.02$ and 0.05 respectively, Figure 6.3A). *PROK2* also increased with gestation, with a significant increase in expression between first and early second trimester (0.1 ± 0.03 vs $0.6 \pm 0.2 \times 10^{-6}$ relative to *GAPDH*, $p=0.02$). A further significant increase in *PROK2* expression was demonstrated at late second trimester compared to both first and early second trimester (1.2 ± 0.2 vs 0.1 ± 0.03 and $0.6 \pm 0.2 \times 10^{-6}$ relative to *GAPDH*, $p=0.0001$ and 0.03 respectively, Figure 6.3B). *PROKR1* displayed a similar expression pattern to that of *PROK1* with a significant increase specifically in late second trimester in comparison to both first and early second trimester (1.8 ± 0.3 vs 0.7 ± 0.1 and $0.8 \pm 0.1 \times 10^{-7}$ relative to *GAPDH*, $p=0.008$ and 0.007 respectively, Figure 6.3C). Conversely, no change gestational change in expression was determined for *PROKR2* ($p=0.4$, Figure 6.3D). These data demonstrate that both ligands and the PROKR1 receptor are developmentally regulated in the human fetal ovary.

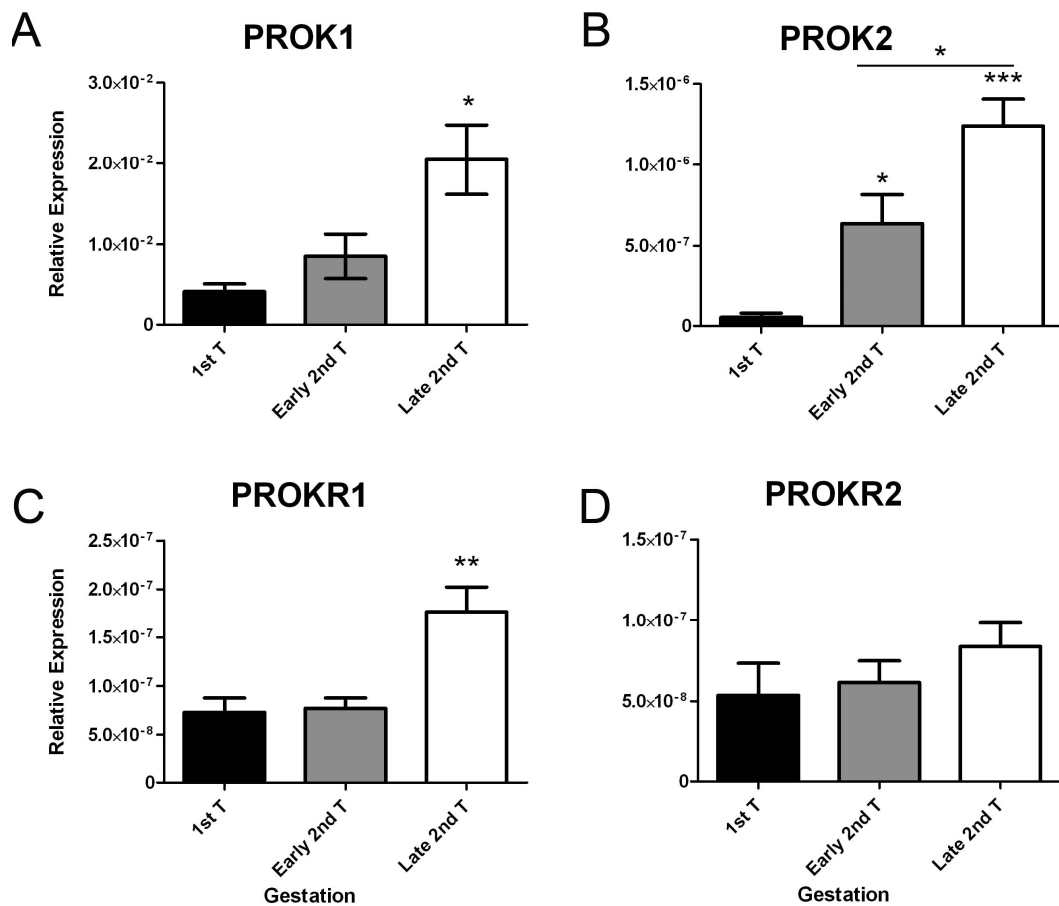


Figure 6.3 *PROK ligand and receptor expression is up-regulated across fetal ovarian development.*

Expression of the two ligands (*PROK1* and 2) and their two shared receptors (*PROKR1* and 2) was analysed by qRT-PCR across gestation and split into age groups; 8-11 weeks (1st T), 14-16 weeks (Early 2nd T), and 17-20 weeks (Late 2nd T; n= 4-6 samples for each gestation). (A) Expression of *PROK1* increased at late 2nd trimester compared to both 1st and early second trimester. (B) *PROK2* expression was up-regulated significantly at each gestation, with late 2nd trimester significantly increased compared to both 1st and early 2nd trimester. (C) *PROKR1* was significantly up-regulated specifically in late 2nd trimester, but (D) no change was seen in *PROKR2* expression. All data are expressed relative to the housekeeping gene *GAPDH*. Significance is determined by one-way ANOVA with Newman-Keuls post-test ($p^* < 0.05$, $p^{**} < 0.01$, and $p^{***} < 0.001$).

6.3.2 PROK ligands localised to the germ cell nests in developing human fetal ovaries

Further characterisation of the PROK ligands was performed via immunohistochemical localisation in the human fetal ovary across a range of gestations. Expression was barely detectable for both ligands in first trimester (data not shown), with increased expression seen in second trimester. PROK1 expression was germ cell-specific, with pairs or groups of germ cells staining intensely compared to other germ cells within the same nest (Figure 6.4A-C). This expression pattern was seen throughout second trimester, with primordial follicles also demonstrating positive PROK1 expression (Figure 6.3 A inset), although not as intense as seen in the earlier germ cells). PROK2 expression was weaker than that of PROK1 with weak expression seen in germ cell nests, including both germ and pre-granulosa cells (Figure 6.4D-F). This expression pattern was seen across second trimester, although definitive staining in primordial follicles was not seen. Negative control tissue incubated without primary antibody confirmed the specificity of the PROK staining, with no positive immunostaining determined (Figure 6.4D inset). These results confirm the protein expression of the PROK ligands mimics that of mRNA, with increasing expression with gestation. The specific intensity of PROK1 in pairs or groups of germ cells suggests it might play a heightened role in these cells.

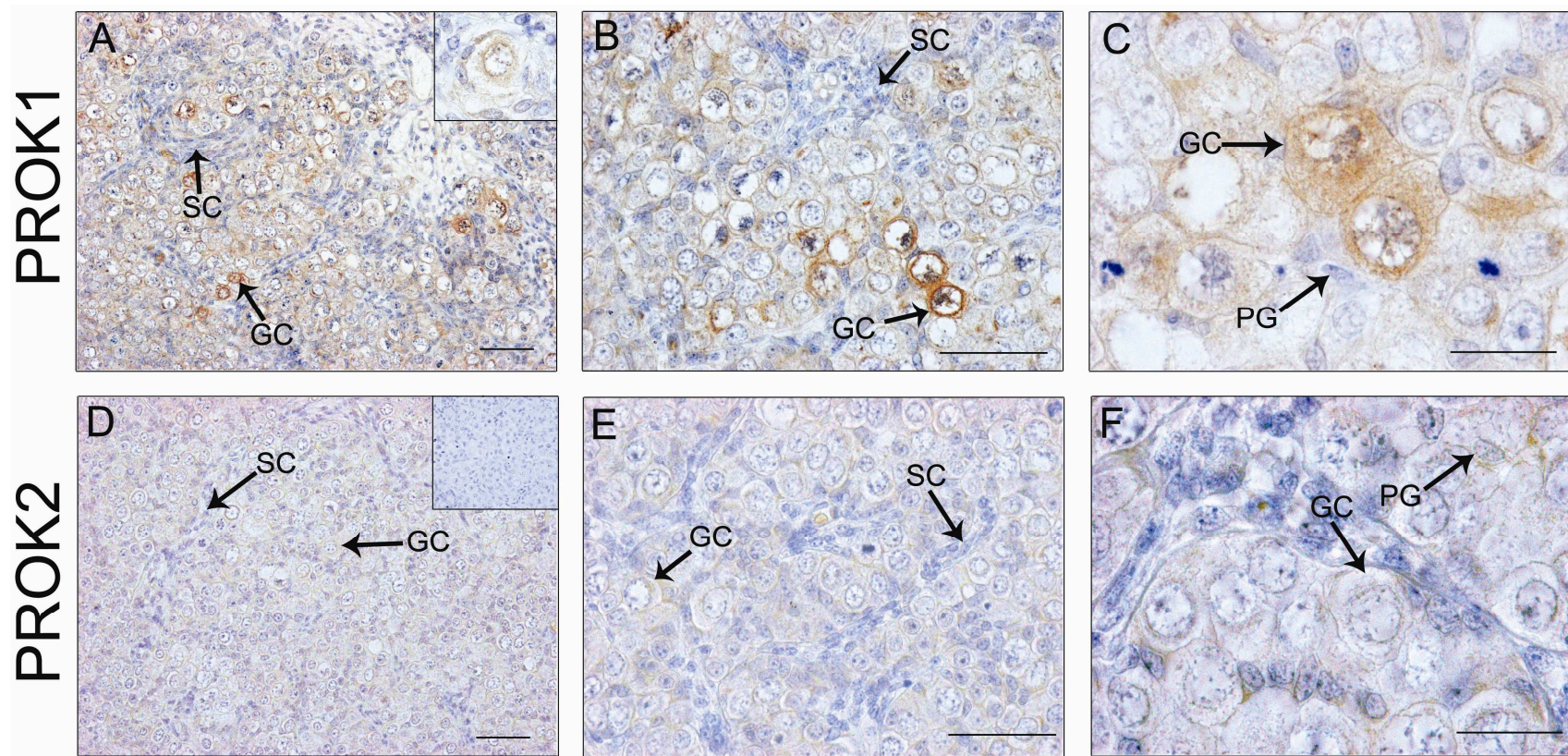


Figure 6.4 *PROK ligands localised to the germ cell nests in the human fetal ovary*

PROK1 and 2 were immunolocalised in the human fetal ovary (14 weeks) using 3,3'-diaminobenzidine tetrahydrochloride staining (brown). (A-C) PROK1 expression was germ cell (GC) specific in the human fetal ovary, with pairs or multiple closely associated germ cells displaying heightened PROK1 expression compared to others nearby. (A inset) PROK1 was also seen in primordial follicles (17 week). (D-F) PROK2 expression was considerably weaker than PROK1 with staining localised to both germ cells and pre-granulosa cells (PG) within germ cell nests, with no staining seen in stromal cell streams (SC). (D inset) No immunolocalisation was seen in negative control tissue in which primary antibody was omitted. Sections were counterstained with hematoxylin and scale bars equal 50 microns in A,B,D, and E; and 20 microns in C and F. Images are representative of staining performed on at least three specimens at roughly the same gestation.

6.3.3 PROK receptors expressed by germ cells of the fetal ovary

In order to determine the targets of PROK action in the human fetal testis the PROK receptors were immunohistochemically located in human fetal ovarian tissue.

PROKR1 was found to be strongly expressed by the germ cells of the fetal ovary, with no staining seen in somatic cell streams or in negative control tissue incubated without primary antibody (Figure 6.5A). Upon closer examination it was apparent that the blood vessels of the human fetal ovary were also positive for PROKR1 (in keeping with its role in angiogenesis) as were some pre-granulosa cells (Figure 6.5B). PROKR2 protein was less distinctly stained, in keeping with lower PROKR2 mRNA compared to PROKR1 (Figure 6.5C). However, staining was apparent in germ cells, with immuno-negative somatic and pre-granulosa cells (Figure 6.5D). These data suggests PROK signalling primarily targets the germ cells of the human fetal ovary, with additional targeting of the blood vessels by PROKR1.

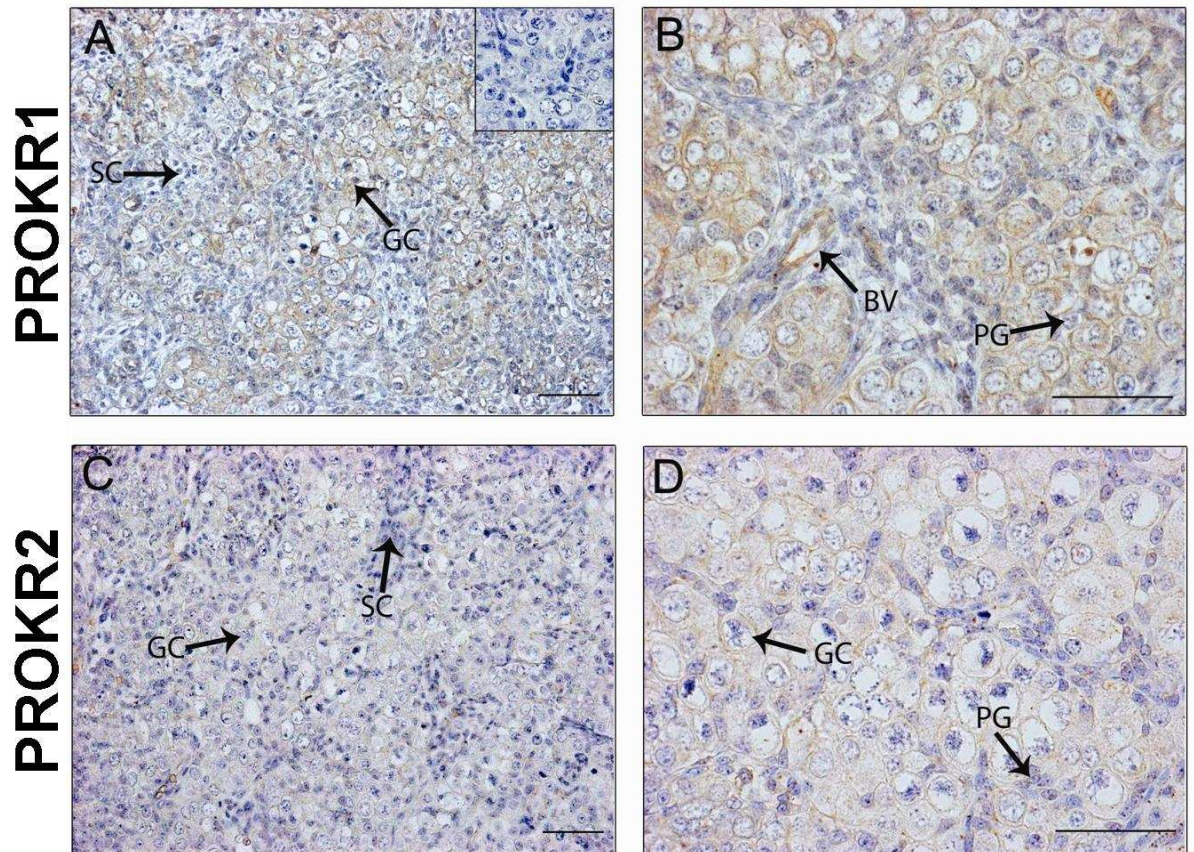


Figure 6.5 *PROK receptor expression in the human fetal ovary*

PROK receptors were immunolocalised in human fetal ovarian tissue (14wk) using 3,3'-diaminobenzidine tetrahydrochloride staining (brown). (A-B) PROKR1 is primarily expressed by fetal germ cells (GC) as well as blood vessels (BV) in the fetal ovary, with some staining of pre-granulosa cells (PG). However, no somatic cell (SC) streams were immuno-negative, as was negative control tissue (A-inset). (C-D) PROKR2 was not intensely expressed by the human fetal ovary, but was apparent in the germ cells. Sections were counterstained with hematoxylin and scale bars equal 50 microns. Images are representative of staining performed on at least three specimens at roughly the same gestation.

6.3.4 T-Cam2 cells stably transfected with PROKR1 as a model for fetal germ cells

As germ cells were determined as the primary target of PROK action, a cell model was created for further investigation of PROK regulation. The TCam-2 cell line have been characterised as a model of fetal germ cells (Young *et al*, 2011), and thus were utilised for this purpose. The cells were initially characterised for expression of the PROK ligands and receptor, but were found to express the PROK receptors at much lower levels than was seen in either the human fetal testis or ovary (as demonstrated later in figure 6.7). For this reason, the TCam-2 cell line was stably transfected with the PROKR1 receptor, as similarly to what was performed previously in the Ishikawa cell line to investigate PROK signalling in endometrial carcinoma (Evans *et al*, 2008).

Initial transfection was performed with both supercoiled and linearised plasmid, as it was unclear which protocol would be most successful in the TCam-2 cells (Figure 6.6A). Positive control plasmid, containing green fluorescent protein (GFP), was simultaneously transfected in order to visually determine positive colonies, which were only seen in cells transfected with supercoiled plasmid (Figure 6.6B-C). These cells were further characterised for continued experimentation.

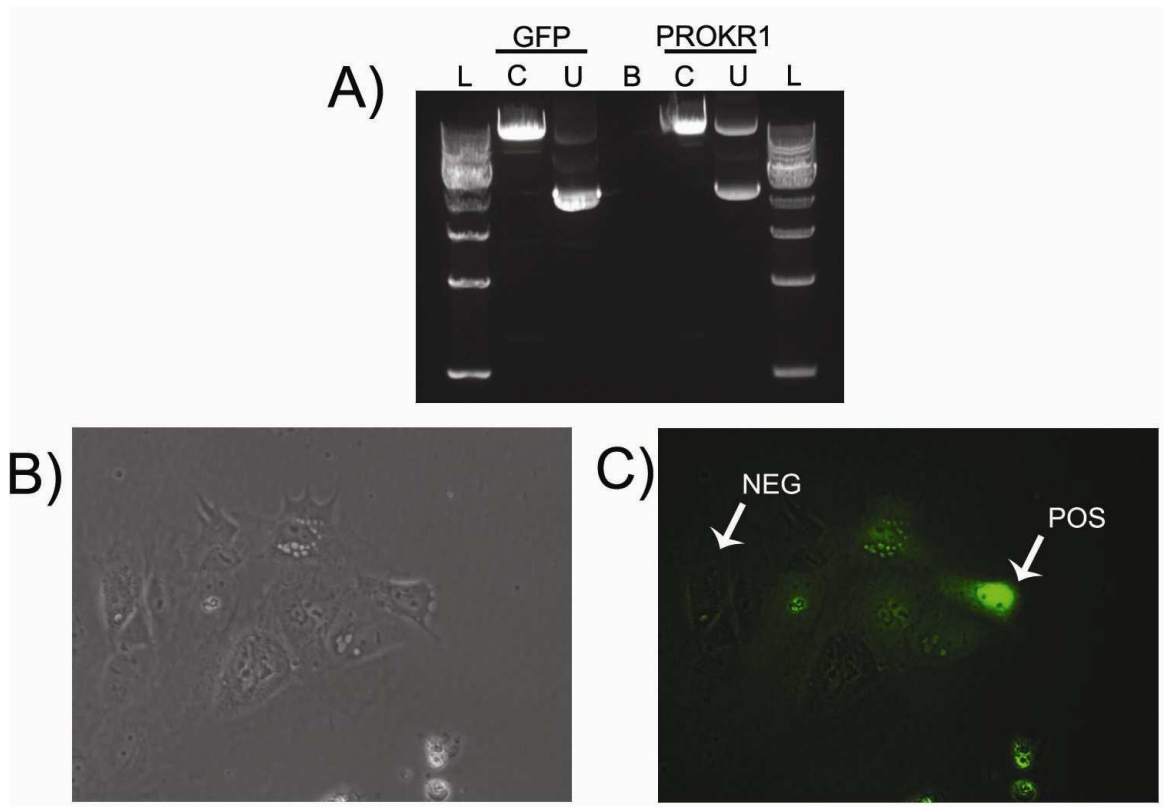


Figure 6.6 *Transfection of TCam-2 cells with PROKR1*

(A) Plasmid containing the PROKR1 gene or GFP was enzymatically cut (C, linearised) or left uncut (U, supercoiled) for transfection of the TCam-2 cell line, and run via electrophoresis to detect successful linearisation as determined by a single high molecular weight band. Uncut plasmid was run alongside, displaying a high molecular weight band (spontaneous linearisation) along with two other bands demonstrating circular and supercoiled plasmid. GFP transfected positive control cells were examined 24 hours post transfection to determine successful transfection. (B) Darkfield microscopy depicting a colony of transfected T-Cam2 cells. (C) The same colony via fluorescent microscopy depicting successful transfection in the form of positively transfected cells (pos) compared to cells negative for GFP (neg).

6.3.5 Characterisation of PROKR1 TCam-2 cells

Before further experimentation, the PROKR1 TCam-2 line was fully characterised to ensure successful transfection. RT-PCR confirmation of increased transcription of *PROKR1* in transfected TCam-2 cells (Figure 6.7A), was further supported by qRT-PCR comparison of PROKR1 TCam-2 cells with untransfected TCam-2 cells, PROKR1 transfected Ishikawa cells and primary human gonadal tissue (Figure 6.7B). Increased expression in TCam-2 cells was also seen at the protein level, as determined via immuno-blotting (Figure 6.7C); this was comparable to levels seen in primary tissue. A second band was seen in the immuno-blot, approximately double the size expected for PROKR1. Although homodimerisation of PROKR2 has been confirmed (Marsango *et al*, 2010), it has only been hypothesised for PROKR1, although this is the likely cause of the larger band, also seen in testis extracts demonstrating the band is physiologically relevant and not an artefact of the cell line. These data determine the transfected TCam-2 cells express *PROKR1* at a heightened level compared to untransfected cells at both the transcript and protein level. This characterization also demonstrates that although *PROKR1* transcript expression in the PROKR1 transfected T-Cam2 line is increased compared to primary tissue, and the protein level expression is comparable to that seen in human fetal gonads.

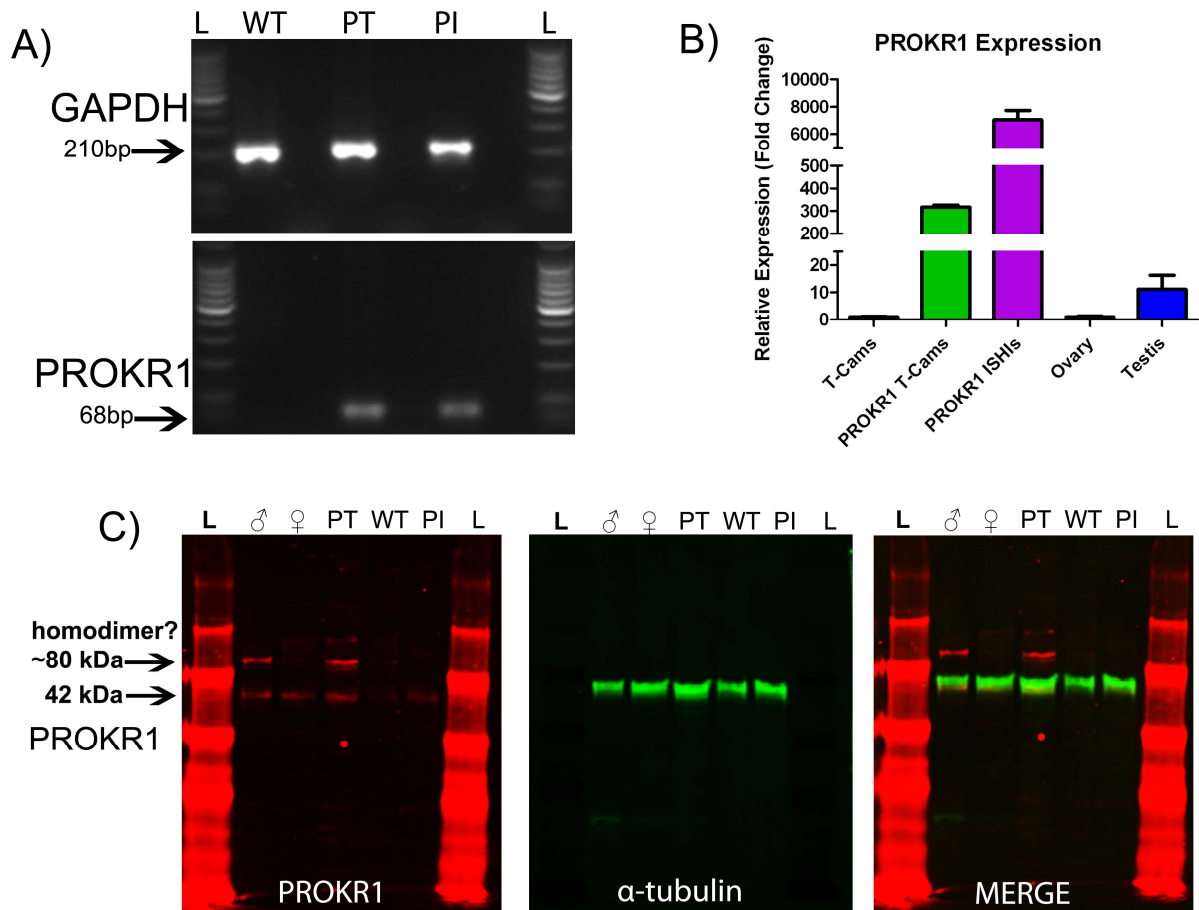


Figure 6.7 Confirmation of transfection of PROKR1 into TCam-2 cells

RT-PCR confirmed increased expression of PROKR1 in PROKR1 transfected TCam-2 cells (PT) compared to wild-type T-Cams (WT). PROKR1 transfected Ishikawa (PI) cells were run alongside as a positive control. B) Quantitative RT-PCR further distinguished this heightened expression in comparison to primary tissue. C) Protein expression was also heightened compared to fetal ovarian (♀) and testicular (♂) tissue. Additionally, a band double the size of PROKR1 was determined in both PROKR1 TCam-2 cells and human fetal testis.

6.3.6 PROK regulation in model germ cells

Previous studies of PROK signalling in the endometrium have suggested PROK is able to regulate both the PGs and the IL-6 type cytokines. Initial investigation of this relationship in fetal germ cells was performed in untransfected/wild-type and PROKR1 transfected TCam-2 cells treated with 40nM PROK1 for 12 hours (n=6). No change was seen in any of the genes examined in untransfected cells, consistent with low expression of the PROK receptors before transfection.

PROKR1 transfected TCam-2 cells displayed a significant increase in *COX2* transcript levels compared to untransfected cells (2.4 ± 0.8 vs $6.9 \pm 2.4 \times 10^{-6}$ relative percentage compared to the housekeeping gene *RPL32*, $p = 0.011$, Figure 6.8A). However, no subsequent increase in the PGE₂ specific enzyme *PTGES* was seen (Figure 6.8B). Despite evidence in other reproductive tissues, no significant up-regulation of any of the IL6-type cytokines was found (Figure 6.8C-F). In contrast, both *IL6* and *LIF* in transfected cells showed a trend for reduced expression, however this was not significant. These data confirm PROK1 via PROKR1 is able to regulated *COX2* expression in an *in vitro* model of fetal germ cells. Additionally, unlike regulation seen in other tissues, the IL6-type cytokines do not respond to PROK1 treatment.

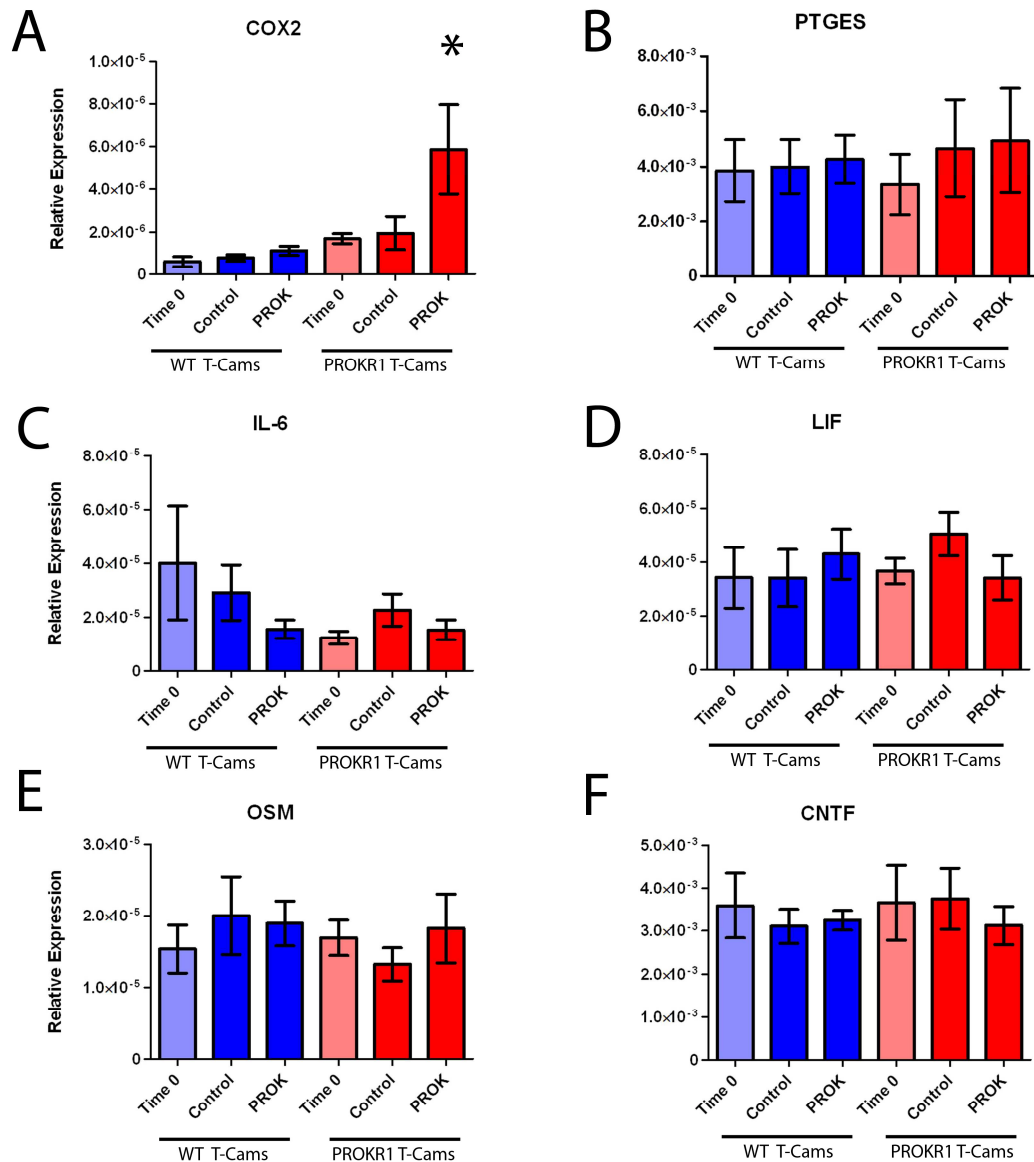


Figure 6.8 Gene expression changes in PROKR1 transfected TCam-2 cells with PROK1 treatment.

Wild-type TCam-2 cells (WT T-Cams) and TCam-2 cells stably transfected with the PROKR1 gene (PROKR1 T-Cams) were treated for 12h with (PROK) or without (Control) 40nM PROK1 and gene expression changes evaluated compared to control (Time 0). (A) The prostaglandin precursor enzyme COX2 was significantly up-regulated when compared to PROK1 treated WT T-Cams, PROKR1 Time 0, and PROKR1 Control (12h untreated). No significant change was seen with treatment in (B) PTGES, (C) IL6, (D) LIF, (E) OSM, or (F) CNTF. (*= $p < 0.05$)

6.3.7 PROK1 regulation of PG signalling components

As initial treatment of cells with PROK1 led to a significant change in COX2 at 12 hours, a full time course was performed on several PG pathway components to identify when up-regulation of gene expression was occurring and what other signalling components might be regulated. In particular, the receptors localised to human fetal germ cells were investigated, as some of the EP receptors have been shown to work in a positive feedback loop with COX2. PROK1-treated (40nM) and untreated PROKR1 transfected TCam-2 cells were collected 2, 4, 8, 12, and 24 hours after treatment along with time 0 control (n=6).

In addition to confirming *COX2* up-regulation at 12 hours, further timecourse analysis determined significant up-regulation at 4 and 8 hour time points (4 hours: 1.6 ± 0.6 vs $3.2 \pm 0.9 \times 10^{-6}$ relative to *RPL32*, $p=0.02$, 8 hours: 2.6 ± 0.6 vs $5.0 \pm 1.6 \times 10^{-6}$ relative to *RPL32*, $p=0.03$, Figure 6.9A). None of the other PG precursor enzymes (*COX1* and *PTGES*) were significantly up-regulated with PROK1 treatment (Figure 6.9B-C). Similarly, the three PGE₂ receptors localised to fetal germ cells; *EP2*, *3* and *4*, were not significantly up-regulated with PROK1 treatment (Figure 6.9D-E). Interestingly, it does appear that *EP3* may be up-regulated in response to continued serum starvation (Figure 6.9E). These data determine PROK1 is able to up-regulate *COX2* specifically, and does not initiate a positive feedback loop of PGE₂ signalling in this system modelling human fetal germ cells.

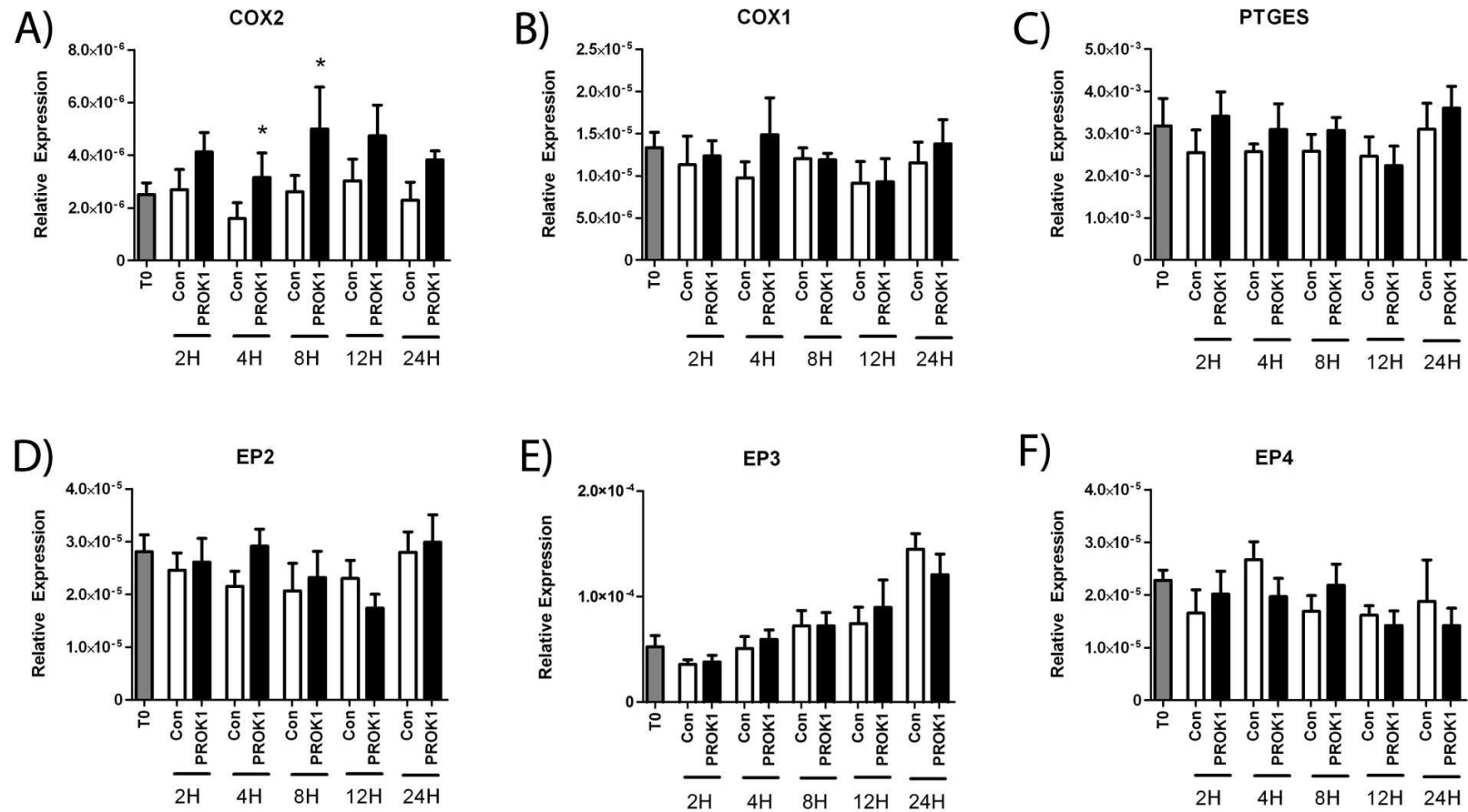


Figure 6.9 Specific up-regulation of COX2 compared with other prostaglandin signalling components

Timecourse analysis of gene expression changes of prostaglandin signaling components after 40nM PROK1 treatment, at time 0 (T0), 2, 4, 8, 12, and 24 hours (H). (A) COX2 is significantly up-regulated with PROK1 treatment after 4 and 8 hours compared to control. No change is seen in the other prostaglandin precursor enzymes (B) COX1 and (C) PTGES. Additionally, no change is seen in the PGE₂ receptors expressed by the germ cells (D) EP2 (E) EP3 or (F) EP4. *p<0.05.

6.4 Discussion

Identifying novel regulators of fetal ovarian development is essential for further understanding of the processes which occur leading up to primordial follicle formation. Fetal ovarian development is critical for adult fertility, thus making regulators of these processes are key to female reproduction. The PROKs are recently identified proteins which have been demonstrated to regulate various other components of the female reproductive system, including the endometrium (Battersby *et al*, 2004; Evans *et al*, 2008; Evans *et al*, 2009), placenta (Hoffmann *et al*, 2006; Hoffmann *et al*, 2007; Denison *et al*, 2008), and fallopian tube (Shaw *et al*, 2010a; Shaw *et al*, 2010b; Shaw *et al*, 2011). Additionally, studies have identified that PROKs may play a role in regulation of the granulosa cells in the adult ovary (Kisliouk *et al*, 2003; Fraser *et al*, 2005).

However, this study is the first to examine possible roles for the PROKs during fetal ovarian development. In doing so, it has been determined that all PROK ligands and receptors are expressed in the human fetal ovary and that expression of both *PROK1* and 2 ligands and *PROKR1* are up-regulated with human ovarian development leading to primordial follicle formation. Unlike in the adult ovary, where most PROK expression is restricted to the granulosa cells (Kisliouk *et al*, 2003; Fraser *et al*, 2005), PROK ligands and receptors were predominantly localised to the fetal germ cells. Additional expression was seen in vascular endothelial cells, which is unsurprising based upon PROK's well identified role in angiogenesis (LeCouter *et al*, 2001; LeCouter & Ferrara, 2003; Tanaka *et al*, 2006). With primary expression of the PROK components in germ cells it is likely that signalling is autocrine or paracrine between other germ cells.

As PROK signalling is predominately restricted to one cell type, we further examined function of the PROKs using a model cell line for primordial germ cells, the T-Cam2 cells. Despite expression of several classical pluripotent and germ cell markers, the T-Cam2 cells only endogenously expressed low amounts of either PROK receptors. In order to circumvent this, the T-Cam2 line was stably transfected with the *PROKR1* gene, as this receptor was previously shown to be both developmentally regulated and more highly expressed in the fetal ovary in

comparison to *PROKR2*. This stably transfected germ cell line further identified PROK1 via PROKR1 signalling is able to up-regulated the prostaglandin precursor enzyme *COX2* specifically, and that this ligand-receptor signalling does not regulate IL6-type cytokine expression in the germ cells, as was shown previously in other cells and tissues (Evans *et al*, 2009; Cook *et al*, 2010).

PROK1 signalling via PROKR1 was able to induce COX2 signalling but did not further affect any of the other prostaglandin enzymes or receptors investigated. This is in contrast to a study which was able to discern up-regulation of EP4 with PROK1 treatment (Wade *et al*, 2010). These data suggest that PROK1, by selectively signalling to COX2 over COX1, may be involved specific events in the fetal ovary rather than homeostatic function, as COX2 is the inducible enzyme which is expressed in response to cytokine signalling (Otto & Smith, 1995; Herschman, 1996). Further, COX2 seems to be important for germ cell development, as demonstrated in the previous study regarding paracetamol exposure during fetal development (as paracetamol is thought to act primarily via inhibition of COX2, Chapter 4). However, the exact downstream effects of COX2 upon up-regulation by PROK1 remains unknown, with data presented here suggesting function downstream of PROK1 signalling may not be via PGE₂ in fetal germ cells. However, it is also possible that significant up-regulation of PGE₂ components was not detected in this study due to limitations of this cell line, and further exploration in primary tissue would be informative.

Additionally, it is possible that the PROK1 may regulate a different COX2-related prostaglandin other than PGE₂, such as PGF_{2α} or PGD₂. There is evidence that PGD₂ plays a role in early gonad development during sex determination (Malki *et al*, 2005; Wilhelm *et al*, 2005); however, little is known about the localisation or function of PGD₂ or PGF_{2α} in regards to germ cell development. Data from other systems also suggests PROK1 is also able to regulate other downstream prostanoids, such as thromboxanes or prostacylin (Wade *et al*, 2010) which may be downstream of PROK1 and COX2 up-regulation in fetal germ cells.

Interestingly, PROK1 was not shown to up-regulate the IL6-type cytokines in this study. Previous investigation in the human reproductive tract demonstrated a regulatory relationship between PROK1 and LIF specifically (Evans *et al*, 2009). In addition, although protein localisation of the other IL6-type cytokines investigated in this study remains unknown in the human fetal ovary (IL6, OSM, CNTF), there is data to suggest LIF is expressed by the fetal oocytes in the human (Abir *et al*, 2004). This demonstrates PROK1 regulation of LIF in germ cell cultures is physiologically relevant. However, PROK1 did not regulate any of the IL6 type cytokines in the PROKR1 T-Cam2 cells, suggesting this signalling pathway may not play a role in early germ cell development.

Several other possibilities may explain the lack of PROK1 regulation of these factors in the PROKR1 T-Cam2 cells. Firstly, LIF localisation has only been performed in human fetal ovaries from 19 weeks gestation onwards (Abir *et al*, 2004). Previous study of the T-Cam2 cells has identified that they more closely resemble germ cells from first trimester specimens (Eckert *et al*, 2008; Young *et al*, 2011; Childs *et al*, unpublished), which may not express LIF protein or the other IL6 type cytokines at physiologically relevant levels (although transcript expression of each was confirmed). Further, although T-Cam2 cells do express early PGC markers, they were derived from male origin and thusly may not respond in the same fashion as germ cells generated from female specimens. No data have been collected regarding IL6-type cytokine expression in the testis, so it is reasonable to conclude there may be gender differences in expression and function of these factors. Additionally, as functional data was gathered from a germ cell specific line, it is possible that PROK1 regulates these factors in another cell type in the fetal ovarian tissue, namely vascular endothelial cells.

In conclusion, this study has examined the newly characterised regulatory proteins PROK1 and 2 in the human fetal ovary across early gestation. We have determined that both ligands and one of their shared receptors, *PROKR1*, are developmentally up-regulated leading to primordial follicle formation and that all components are primarily expressed by the fetal germ cells suggesting autocrine signalling or paracrine signalling between germ cells. However, there is also evidence for

expression in the endothelial cells of the vasculature suggesting PROKs may play a role in angiogenesis, for which they are well characterised in other tissues. Further functional characterisation was performed on a novel PROKR1 stably transfected human germ cell line, in order to determine downstream targets of PROK1 signalling and possible function in germ cells. These studies determined that PROK1 is able to consistently regulate the prostaglandin precursor enzyme COX2, which is implicated in germ cell survival in previous chapters (Chapter 3 and 4). Together these data suggest a novel role for PROKs in the human fetal ovary in the regulation of COX2 and possible downstream targets to promote pathways such as survival and/or angiogenesis. However, additional investigation is needed in primary tissue to further discern further exact function of the PROK ligands during human fetal ovarian development.

Chapter 7

Prokineticins in fetal testis development

Chapter 7. Prokineticins in fetal testis development

7.1 Introduction

PROKs function to promote angiogenesis, proliferation, and migration in various reproductive organs (reviewed in (Maldonado-Perez *et al*, 2007) and discussed in detail in Section 6.1) but have yet to be described in the fetal testis. Early characterisation of the PROKs identified they were active in steroidogenic organs of the body, including the prostate and the testis (Wechselberger *et al*, 1999; LeCouter & Ferrara, 2003). In fact, in the mouse and rat, the testis is described to have the highest level of *Prok2* expression in the body, although *Prok2*'s best characterised role is in the regulation of the hypothalamus (LeCouter *et al*, 2003). Brief characterisation of PROK expression was also performed in the human testes when examining their possible function in testicular cancer (Samson *et al*, 2004). These studies determined PROK1 ligand is expressed in the Leydig cells of the adult testis rather than in the germ cells as demonstrated in the ovary in the previous chapter (LeCouter *et al*, 2003; Samson *et al*, 2004). Further, gene expression array analysis of gonads from both male and female mice determined there were differential expression patterns of some of the PROK signalling components during ovarian and testicular development (Menke & Page, 2002). This differential localisation and transcript expression, along with the heightened expression of PROK2 in the testis compared to the rest of the body, led to the hypothesis that the PROKs might play a role during early testicular development.

In the fetal testis, like the fetal ovary, several developmental processes take place in a complex and highly organised fashion in order to form a functional gonad for future adult fertility. Male sex determination (as described in Section 1.3) occurs early in gestation, with testis differentiation becoming evident at ~week 8 of gestation in the human (Anderson *et al*, 2002a). Testis development is initiated after Sertoli cell differentiation, which has been hypothesised to be the rate limiting step in further differentiation of other testicular cell types (Wilhelm *et al*, 2007). Developing Sertoli cells appear to regulate a cascade of developmental and morphological changes in the testis via several growth factors. One such factor is Anti-Müllerian

hormone (AMH), which is expressed by the differentiating Sertoli cells subsequent to SRY expression (Hacker *et al*, 1995) at ~8 weeks gestation in the human (Rajpert-De Meyts *et al*, 1999; Barbara *et al*, 2000). Sertoli cells then migrate and associate with germ cells to form sex cords (Hughes, 2001). These cords provide the basis for future seminiferous tubules, being the first sign of testis specific differentiation, and after which point the germ cells are referred to gonocytes and pre-spermatagonia (as opposed to oogonia and oocytes in the ovary) (Cooke & Saunders, 2002; Gaskell *et al*, 2004).

AMH released from the Sertoli cells promotes migration of cells from the mesonephros to further colonise the testis (Bezard *et al*, 1987; Behringer, 1995). However, AMH is not thought to be the only factor involved in mesonephros migration (Ross *et al*, 2003). FGF9 is also postulated to aid in regulation of cell migration (Colvin *et al*, 2001). Although the signalling mechanisms governing cell migration to the testis from the mesonephros are poorly understood, it is a process which appears to be essential for further testis cord formation in the rodent (Tilman & Capel, 1999). It is postulated the migratory cells then differentiate and give rise to the peri-tubular myoid (PTM) cells, peri-vascular cells, and a sub-set of the Leydig cells (Merchant-Larios *et al*, 1993; Martineau *et al*, 1997; Merchant-Larios & Moreno-Mendoza, 1998; Nishino *et al*, 2001).

Leydig cells are evident in the human fetal testis from ~8 weeks gestation, and are formed from two distinct sub-sets of progenitors (Codesal *et al*, 1990; Ostrer *et al*, 2007; DeFalco *et al*, 2011). As described above, one of the cohorts of Leydig cell progenitors migrates from a specialised region between the gonad and mesonephros border; while the other cohort of progenitor cells migrates from the coelomic epithelium. Sertoli cells then function in a paracrine fashion, secreting factors to promote Leydig cell differentiation (Karl & Capel, 1998; Ge *et al*, 2006; DeFalco *et al*, 2011). *Pdgfra*, is one such factor secreted by the Sertoli cells, which signals to the interstitial cells in the fetal testis, and interruption of *Pdgfra* signalling leads to Leydig cell disruption (Brennan *et al*, 2003). Another factor with similar function is Desert hedgehog (*Dhh*) (Bitgood *et al*, 1996). In addition to Leydig cell disruption, *Dhh*^{-/-} mice also display poor segregation of the tubules from the interstitial compartment

(Yao & Capel, 2002), suggesting *Dhh* might be involved outwith Leydig cell differentiation. Mutations in *DHH* in humans are associated with fertility disorders, most often gonadal dysgenesis and infertility (Umehara *et al*, 2000; Canto *et al*, 2004; Canto *et al*, 2005), and fetal testes collected from smoking mothers also displayed lowered *DHH* levels (Fowler *et al*, 2008).

Leydig cells regulate further masculinisation of the testis and secondary sex organs via the secretion of androgens (Clark *et al*, 2000; Hu *et al*, 2002; Welsh *et al*, 2007). Testosterone is produced via a several step enzymatic process from cholesterol (as depicted in Figure 7.1). Enzymes produced by the Leydig cells (eg *StAR*, *CYP11A1*), necessary for androgen production, and testosterone itself are detected around the start of Leydig cell differentiation and peak at early second trimester in the human (Tapanainen *et al*, 1981; O'Shaughnessy *et al*, 2007; Scott *et al*, 2009). In addition to androgens, the Leydig cells also produce insulin-like3 (*INSL3*), a factor initially characterised in regulation of testicular descent (Ivell & Hartung, 2003; Klonisch *et al*, 2004). In addition, *INSL3* regulates germ cell survival directly via its receptor leucine-rich repeat-containing G-protein-coupled receptor 8 (*LGR8*) (Kawamura *et al*, 2003).

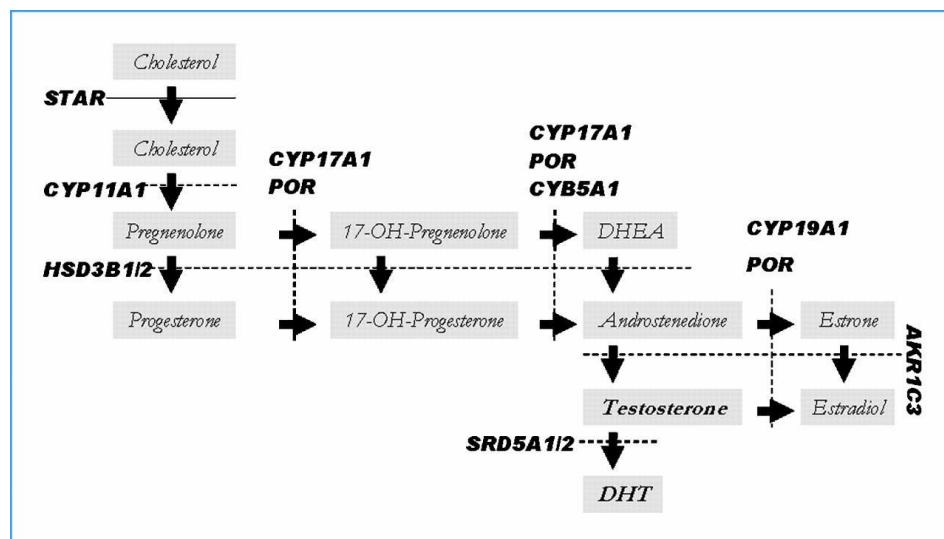


Figure 7.1 Steroid synthesis pathway in the human testis.

The human fetal Leydig cells produce testosterone via the degradation of cholesterol via several enzymatic steps as demonstrated briefly above. Figure from (Hofland *et al*, 2010).

After initial differentiation, the Leydig cells in the fetal testis undergo a proliferative/hyperplastic event from 14-18 weeks, increasing vastly in number, which also correlates with increased steroidogenesis during this time (Codesal *et al*, 1990; Murray *et al*, 2000).

Other cell types to migrate from the mesenphros to the testes are the PTM cells and the perivascular cells (Martineau *et al*, 1997; Nishino *et al*, 2001). Both of these cell types become evident in the human fetal testis at ~12 weeks gestation (Ostrer *et al*, 2007). Once settled in the gonad, the PTM cells differentiate and migrate to surround the germ and Sertoli cell aggregations to form a flattened cell layer providing infrastructure to the seminiferous tubules (Wilhelm *et al*, 2007). In the human, the PTM layer displays tight junctions similar to other connective tissues (Ross & Long, 1966) and demonstrates contractile properties later in adulthood aiding in release of elongated spermatids. Perivascular cells also migrate from the mesenphros to the fetal testis (Nishino *et al*, 2001) and are important for neoangiogenesis. Blood vessel formation is heightened during fetal testis development and aids in trafficking of hormones within the testis and to other organs.

In summary, early fetal testis differentiation is highly organised and composed of several processes including: Sertoli cell differentiation, cord formation and AMH release; migration of multiple cell types to the testis; Leydig cell differentiation, proliferation and initiation of steroidogenesis; PTM differentiation and seminiferous tubule enclosure; and vascular formation (as summarised in Figure 7.2). All of these events are important for the development and support of the gonocytes for future spermatogenesis during adulthood.

Normal differentiation of the testis

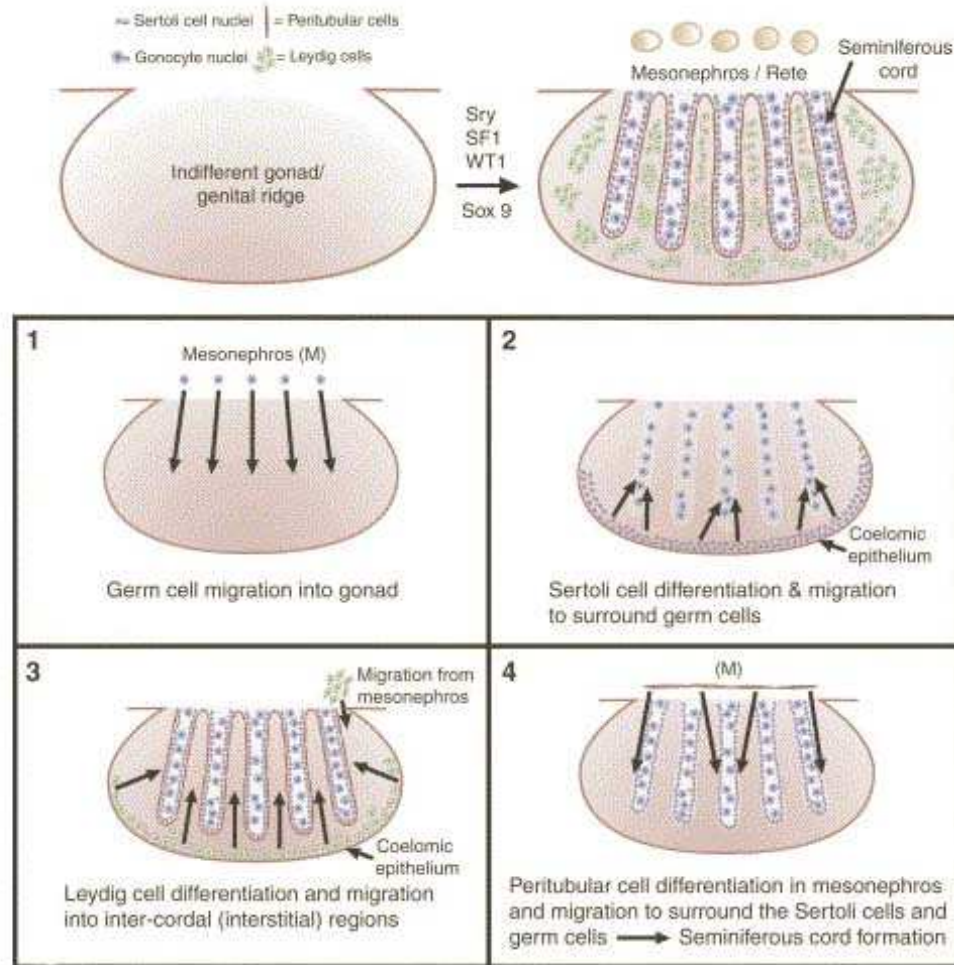


Figure 7.2 Summary of human fetal testis development.

Gonad formation initiates with the 1) migration of the primordial germ cells to the genital ridge. At this point the gonad is bi-potential, but signaling from the SRY gene promotes 2) Sertoli cell differentiation and migration. This is followed by 3) migration of the Leydig cells to the testis from the mesonephros and the coelomic epithelium and promote further testis formation via secretion of androgens. 4) Further migration of peritubular myoid cells and peri-vascular cells form the infrastructure of the fetal testis. Figure adapted from (Sharpe *et al*, 2006).

As in the ovary, little is known about the developmental pathways that regulate testicular formation. The PROKs have been postulated by other groups to be involved in angiogenesis and steroidogenesis, which are two main functions required for testicular growth and development (Wechselberger *et al*, 1999; Samson *et al*, 2004; LeCouter *et al*, 2003). For this reason, the PROK ligands and receptors were characterised in the human fetal testis across early gestation, as was performed in the fetal ovary in the previous chapter. Further dual immunohistochemical staining and cultures were performed in order to extrapolate a possible function for PROK signalling during early male development.

In addition, PROK1 regulation of several factors was investigated, to determine changes in transcript expression. These factors include components from previous studies (the PGE₂ and IL6-type cytokine pathways), components of the steroidogenesis pathway (CYP11A1 and StAR), and factors found to be regulated by PROK1 in previous studies which are thought to be involved in testis development (DKK1 and ID3) (Macdonald *et al*, 2010).

7.2 Materials and Methods

Tissue collection

Human fetal tissue used in the following experiments was obtained and dissected as described previously (Section 2.1), with subsequent SRY genotyping to determine sex of first trimester specimens (Section 2.3).

RNA extraction and cDNA synthesis

Sample tissue was then processed to extract RNA and subsequently synthesis cDNA for genomic analysis as previously discussed (Section 2.4).

Quantitative RT-PCR

In order to determine if mRNA transcripts encoding PROK signalling targets (PROK1, PROK2, PROKR1 and PROKR1) were expressed differentially compared to the fetal ovary and to determine variation across gestation, qRT-PCR was performed using the ABI 7500Fast system and both Sybr Green and Taqman analysis as described in Section 2.5.

Quantitative RT-PCR analysis of fetal interstitial cultures was also performed using the ABI 7900HTFast system and Sybr Green analysis to determine any gene expression changes in possible PROK targets (*PTGES*, *BDNF*, *MCL-1*, *LIF*, *OSM*, *IL6*, *CYP11A1*, *StAR*, and *ID3*) and Taqman analysis was also performed for targets with primer/probe sequences (*COX2*, and *DKK1*), details of this protocol are also outlined in Section 2.5.

Immunohistochemistry

Human fetal testis samples were used to localise PROK ligands (PROK1 and 2) and receptors (PROKR1 and 2) to determine cell-specific sites of PROK synthesis and action. Further staining was then performed with cell specific markers 3 β -HSD (Leydig) and SMA (blood vessels), to confirm cell specificity of the PROK receptors. Finally, immunohistochemistry was also utilised to determine changes in apoptosis (CC3) and proliferation (BrdU). Protocols for these localisations can be found in Section 2.8.

Human fetal testicular culture

Second trimester fetal testes (n= 6, 14-17 weeks gestation) were cultured as small explants in hanging-drop culture as described previously (Zhang *et al*, 2008; Szczepny *et al*, 2009). Tissue was cultured using organ culture media as described in Section 2.13. Tissue was split into two treatment groups; vehicle control (H₂O) or 40nM PROK1. Tissue was cultured for 24 hours for histological analysis and subsequently fixed in Bouins solution and processed as in Section 2.6.

Further examination to determine gene expression changes resulting from PROK1 treatment were performed by differential plating to isolate fetal interstitial cells for culture (n= 6, 14-16 weeks gestation). Testes were disaggregated and cultured overnight in 6-well plates with 0.01% gelatin coating to promote adhesion of interstitial cells. Germ, Sertoli, and Leydig cells did not adhere and were removed 12 hours post-plating, at which time the remaining interstitial cells were treated with 40 nM PROK1 for 24 hours. This allowed for additional isolation of the cells responding to PROK1 treatment, allowing for selective investigation of specific cell response. Interstitial cell cultures were lysed in RLT buffer following culture and snap frozen for further RNA extraction and cDNA synthesis.

Stereology/Image Analysis

Histological changes after PROK1 treatment in the human fetal testis were determined via image analysis using various markers as described in Section 2.11.3.

Measurements of proliferation and apoptosis were performed using two slides from each sample at least 10 sections apart (50 microns). Each slide contained sections from 4-6 pieces of hanging drop tissue. Positive cells (BrdU or CC3) were counted and designated intra- or extra- tubular based upon their localisation within the tissue. Random frames were generated and all cells were counted within the frame until a quantity designated as significant (as determined based upon area of the tissue) by the image analysis software was achieved. These counts were then corrected for area of the whole tissue and tubular area.

Statistical Analysis

Quantitative RT-PCR data were analysed with GraphPad Prism version 4 statistical software (GraphPad Software Inc). Gestational comparison data were analysed using one-way ANOVA, data were then either analysed as described or log-transformed for further analysis. Log-transformation was performed in instances where data sets did not fit a Gaussian distribution. The Kolmogorov-Smirnov normality test was used for this purpose.

Data were then analysed utilising the Newman-Keuls Multiple Comparison post-test to determine significant changes between gestational values. This post-test was chosen as has more strength than a Tukey post-test and the risk of type I error does not occur with only three groups (as in our study). Some data was also analysed using a post-test for linear trend, this test was performed when data looked to be in a natural order (increasing or decreasing across gestation).

Gene expression changes identified using qRT-PCR after PROK1 treatment of human fetal testes were also analysed using GraphPad Prism as above. Data were analysed using paired t-tests comparing PROK1 treated tissue to dH₂O treated tissue (as the appropriate control).

7.3 Results

7.3.1 Genes encoding PROK signalling components are developmentally-regulated in the fetal testis

To determine presence and pattern of expression of the two PROK ligands and their shared receptors during human fetal testis development, qRT-PCR was performed across a range of gestations. Testis samples were split in three gestational groups, similar to what was performed for ovarian gestational analysis in previous chapters. In the testis these ages also equate to developmental events: 1st trimester (8-10 weeks), Sertoli cell differentiation; early second trimester (14-16 weeks), Leydig cell migration, differentiation, and testosterone secretion; and late second trimester (17-21 weeks) PTM and peri-vascular cell differentiation and Leydig and germ cell proliferation.

Transcripts encoding all four PROK signalling components were detected in the human fetal testis across all gestations examined. Expression of *PROK1* was significantly increased in early and late second trimester compared to first trimester (4.1 ± 1.2 and 3.9 ± 1.4 vs 0.4 ± 0.1 relative expression compared to the housekeeping gene *GAPDH*, $p=0.009$ and 0.04 respectively, Figure 7.3A). *PROK2* expression increased linearly across gestation, with increased expression between first to early second trimester (0.2 ± 0.04 vs $1.7 \pm 0.5 \times 10^{-2}$ relative to *GAPDH*) and again between early second and late second trimester (1.7 ± 0.5 vs $3.3 \pm 0.7 \times 10^{-2}$ relative to *GAPDH*, linear trend $p=0.005$, Figure 7.3B). Messenger RNA expression of both PROK receptors (*PROKR1* and 2) displayed similar expression patterns across gestation, with significant increases in expression specifically at late second trimester compared to both first and early second trimester (*PROKR1* = 0.7 ± 0.1 and 0.6 ± 0.1 vs $1.3 \pm 0.1 \times 10^{-2}$ relative to *GAPDH*, $p=0.009$ and 0.007 respectively, Figure 7.3C) (*PROKR2* = 2.4 ± 0.7 and 1.5 ± 0.6 vs $9.6 \pm 2.0 \times 10^{-3}$ relative to *GAPDH*, $p=0.01$ for both comparisons, Figure 7.3D). These data demonstrate that mRNA expression of both PROK ligands and receptors is increased with testis development.

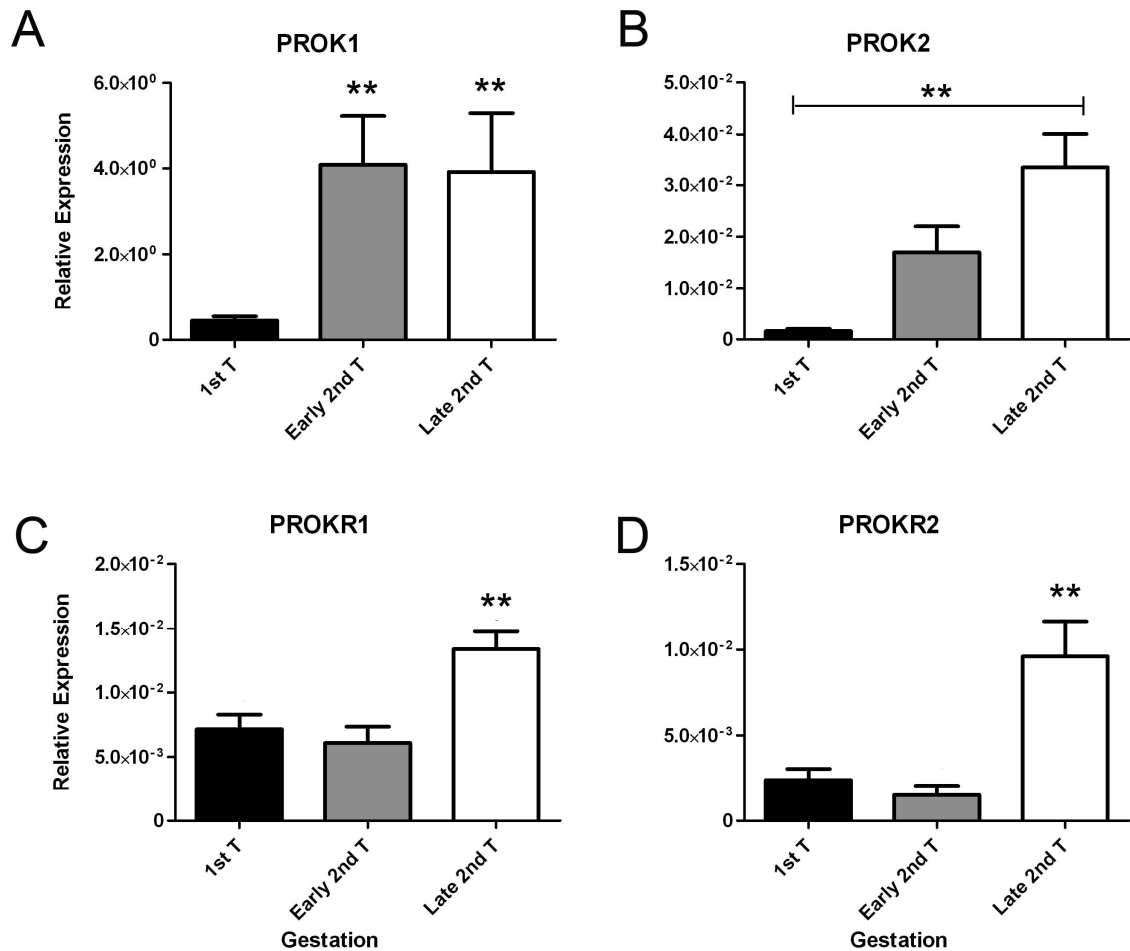


Figure 7.3 *Messneger RNA expression of PROK components is up-regulated with development in the fetal testis*

Expression of the two ligands (PROK1 and 2) and their two shared receptors (PROKR1 and 2) was analysed by qRT-PCR across gestation and split into age groups; 8-10 weeks (1st T), 14-16 weeks (Early 2nd T), and 17-21 weeks (Late 2nd T; n= 4-6 samples for each gestation). (A) Expression of PROK1 increased between 1st trimester and both early and late 2nd trimester (**=p<0.01). (B) PROK2 expression was significantly up-regulated across gestation (**=p<0.01, determined by test for linear trend). (C) PROKR1 and (D) PROKR2 expression were significantly up-regulated specifically in late 2nd trimester (**=p<0.01). All data are expressed relative to the housekeeping gene *GAPDH*. Significance is determined by one-way ANOVA with Newman-Keuls post-test, except in the case of PROK2 which was determined by post-test for linear trend.

7.3.2 PROK ligands are expressed in most cell types of the human fetal testis

DAB immunohistochemical detection was performed to determine sites of PROK ligand protein expression in the human fetal testis. PROK1 expression was diffuse with expression seen both within the seminiferous cords and in the interstitial compartment of the fetal testis (Figure 7.4A and B). PROK1 expression was also seen in blood vessels of the human fetal testis. PROK1 expression does appear to be specific, as control tissue from the endometrium was run with the same concentration of primary antibody and clearly displays immuno-negative stromal cells along with immuno-positive glandular tissue (Figure 7.4 inset). PROK2 expression was more restricted, with the interstitial compartment being the primary site of PROK2 expression (Figure 7.4C and D). Weak staining was also seen within seminiferous cords but was not seen in the epithelium. Negative control tissue incubated without primary antibody was run alongside both PROK1 and 2 and detected no non-specific staining. In comparison to second trimester, tissue from first trimester specimens did not readily express either ligand (data not shown), suggesting PROK protein expression is lower in earlier ages, similar to that of PROK transcript expression. These data suggest PROK1 is highly expressed in the human fetal testis and is not restricted to a specific cell type, whereas PROK2 is also highly expressed, but is primarily expressed by Leydig and interstitial cells in the interstitial compartment of the fetal testis.

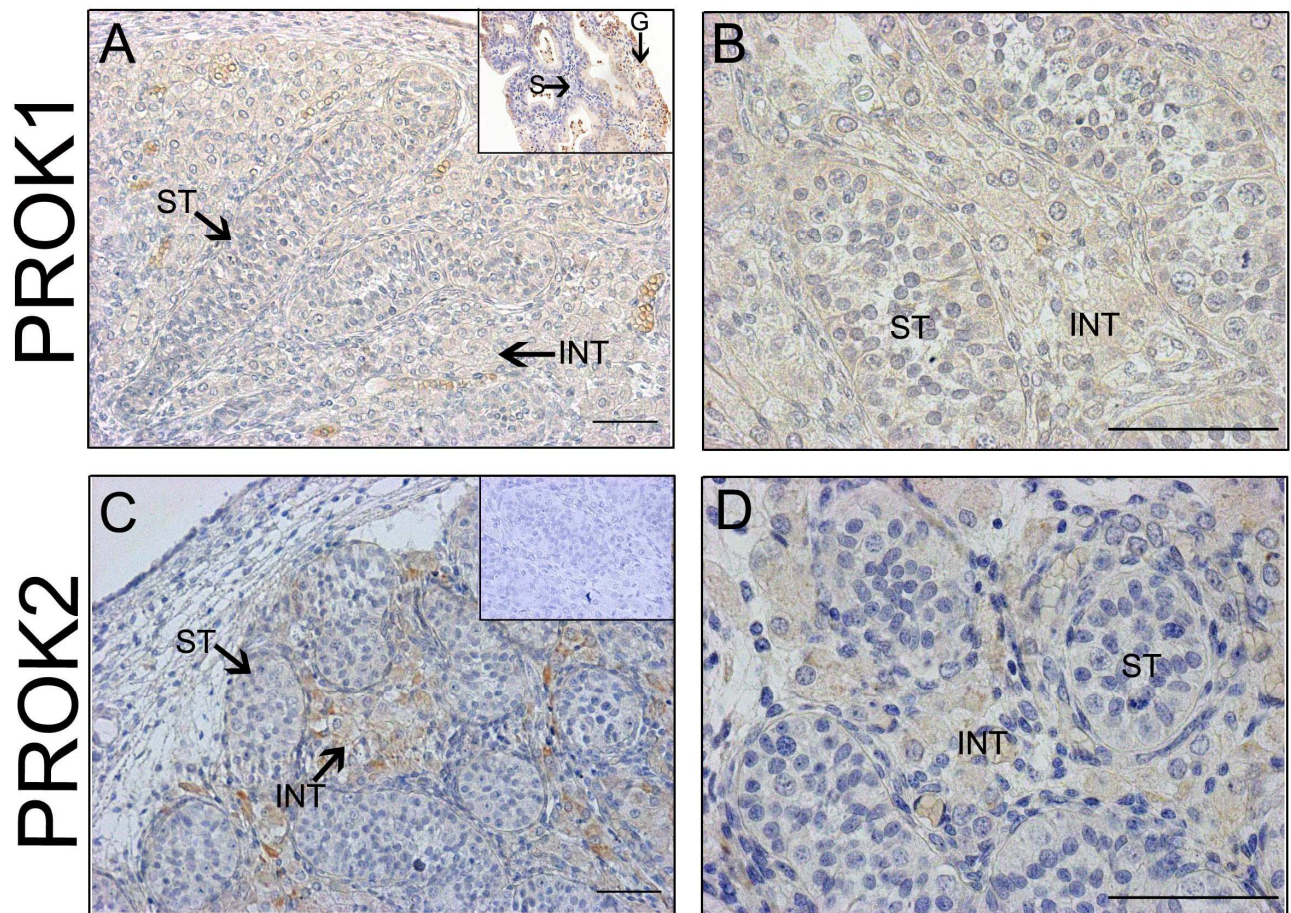


Figure 7.4 *PROK1 and 2 are highly expressed in the human fetal testis*

Immunohistochemistry was performed for PROK1 and 2 in 15 week human fetal testis tissue. (A-B) 3,3'-diaminobenzidine tetrahydrochloride staining (brown) determined PROK1 expression was diffuse throughout the fetal testis, localised both in the seminiferous cords (ST) as well as the interstitial compartment (INT). (A inset) This localisation appears to be specific as the same concentration of primary antibody stained glandular tissue (G) but not stroma (S) in endometrial control tissue. (C) PROK2 was primarily localised to the interstitial compartment of the human fetal testis (D) with weak expression seen within the seminiferous cords. (C inset) No staining was determined in the negative control testis tissue incubated without primary antibody. All scale bars equal 50 microns. Images are representative of staining performed on at least three specimens at roughly the same gestation.

7.3.3 PROK receptors localised to the interstitial compartment of the human fetal testis

Fluorescent immunohistochemistry was utilised to determine the protein expression of the two PROK receptors (PROKR1 and 2) in the human fetal testis. Both receptors displayed similar sites of expression, with marked expression within the interstitial compartment of testis but no expression within the cords (Figure 7.5 A-B). However, it was noted that not all cells within the interstitial compartment were immuno-positive for either PROKR1 or PROKR2. These results suggest the two receptors may be specific to certain cell type, most likely being either Leydig or other interstitial cells.

In order to determine the site specific expression of the two receptors, each was fluorescently co-localised with the Leydig cell marker 3 β -HSD (an enzymes utilised in steroid synthesis). PROKR1 did not display any co-localisation with 3 β -HSD, demonstrating its primary site of localisation in the human fetal testis to be the non-Leydig interstitial cells (Figure 7.6). Conversely, PROKR2 was highly co-localised with 3 β -HSD, signifying PROKR2 is primarily expressed by the Leydig cells of the human fetal testis (Figure 7.6). These data indicate the PROK receptors are both expressed within the interstitial compartment of the fetal testis making this the primary site of PROK ligand action; however, the receptors are expressed on differing cell types, with PROKR1 targeting non-Leydig interstitial cells and PROKR2 targeting the Leydig cells. In addition, expression of both receptors increased with gestation, in keeping with transcript expression data.

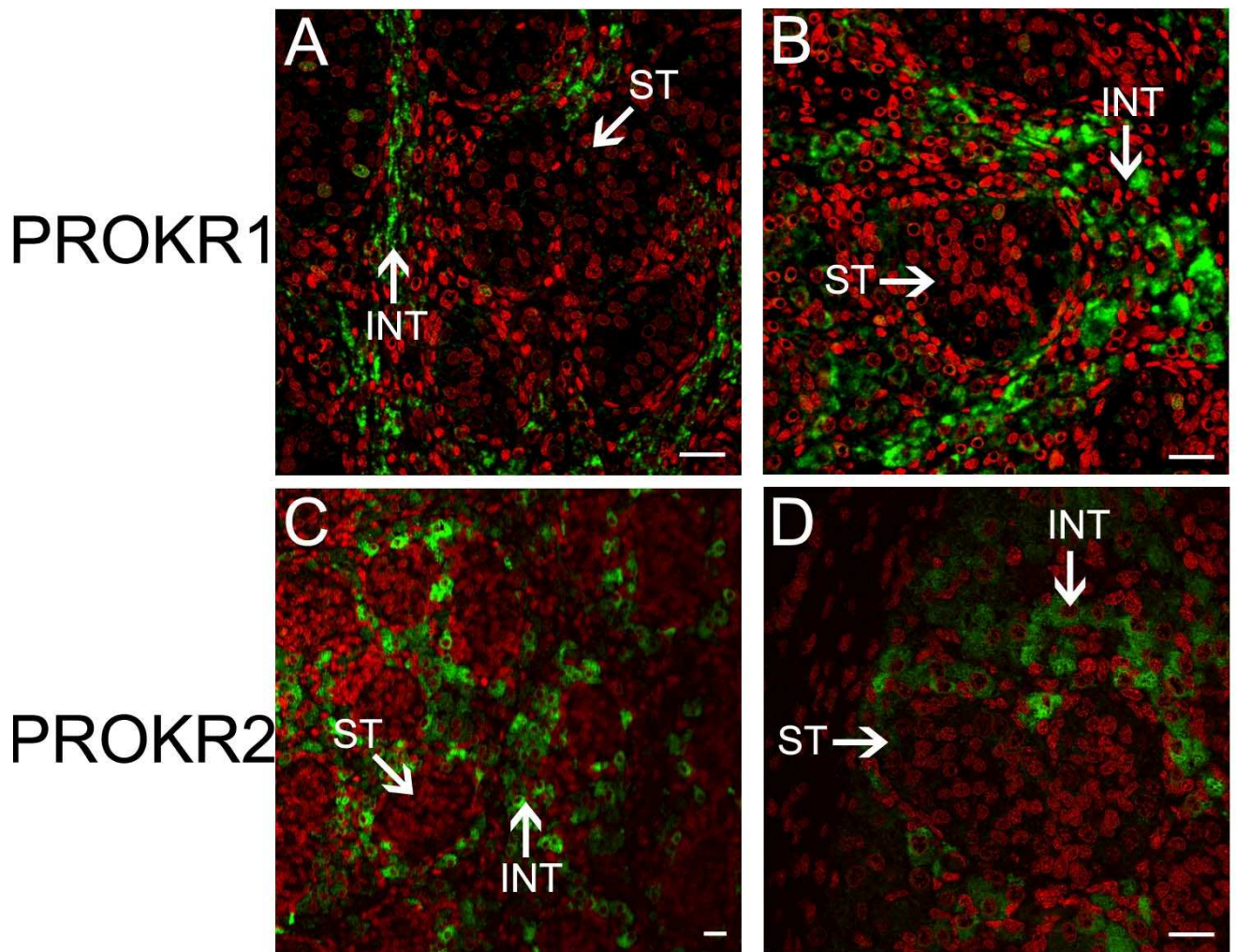


Figure 7.5 *PROK receptor expression restricted to interstitial compartment of the human fetal testis*

Fluorescent immunohistochemical detection of the PROK receptors (green) in 18 week human fetal testis tissue. (A-B) PROKR1 is restricted to the interstitial compartment (INT) of the human fetal testis with no expression determined in the seminiferous tubules (ST) as is (C-D) PROKR2. Not all cells in the INT are expressing the receptors suggesting a possible cell-specific target. Propidium iodide used as a nuclear counterstain (red). Scale bars equal 20 microns. Images are representative of staining performed on at least three specimens at roughly the same gestation.

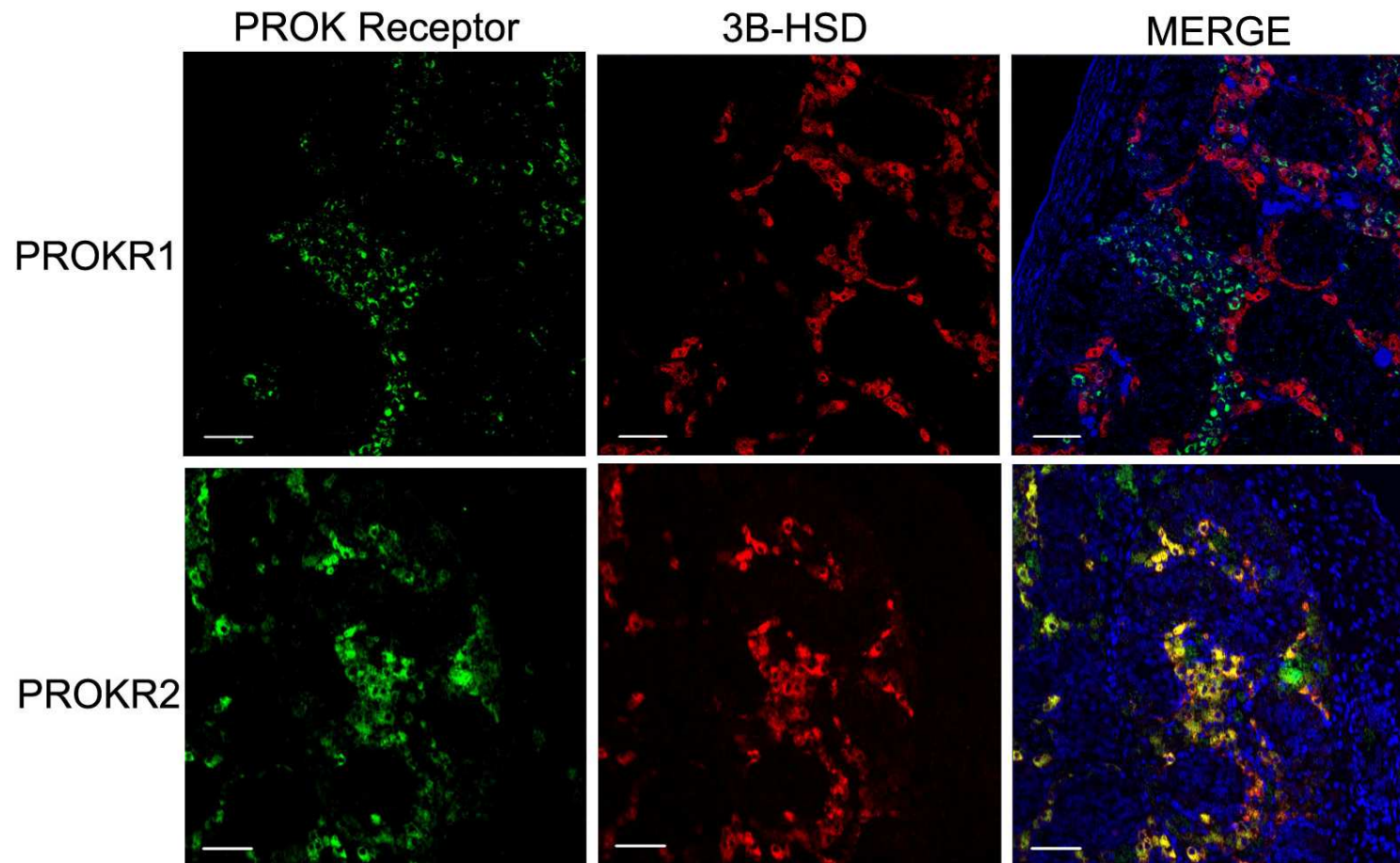


Figure 7.6 Co-localisation of PROK receptors with Leydig cell marker 3 β -HSD

Fluorescent immunohistochemical localisation in 18 wk human fetal testis of PROK receptors (green) with Leydig cell marker 3 β -HSD (red). (A) PROKR1 does not co-localise with 3 β -HSD, and is therefore restricted to the non-Leydig cells of the human fetal testis. (B) PROKR2 does co-localise with 3 β -HSD, demonstrating Leydig cells are the primary site of PROKR2 signalling. DAPI counterstain (blue) was utilised. Scale bars equal 50 microns. Images are representative of staining performed on at least three specimens at roughly the same gestation.

7.3.4 PROK receptors expressed by fetal testicular vasculature

PROK receptor localisation was also investigated in fetal vasculature. The vascular marker α -smooth muscle actin (SMA) was utilised to identify blood vessels within human fetal testis tissue. Both PROKR1 and 2 displayed distinct co-localisation with SMA throughout later gestations (distinct vasculature is not apparent until late second trimester, Figure 7.7). These data determine PROK signalling may play a classical role in neo-angiogenesis in the testis as well as a possible role with interstitial cells in the human fetal testis.

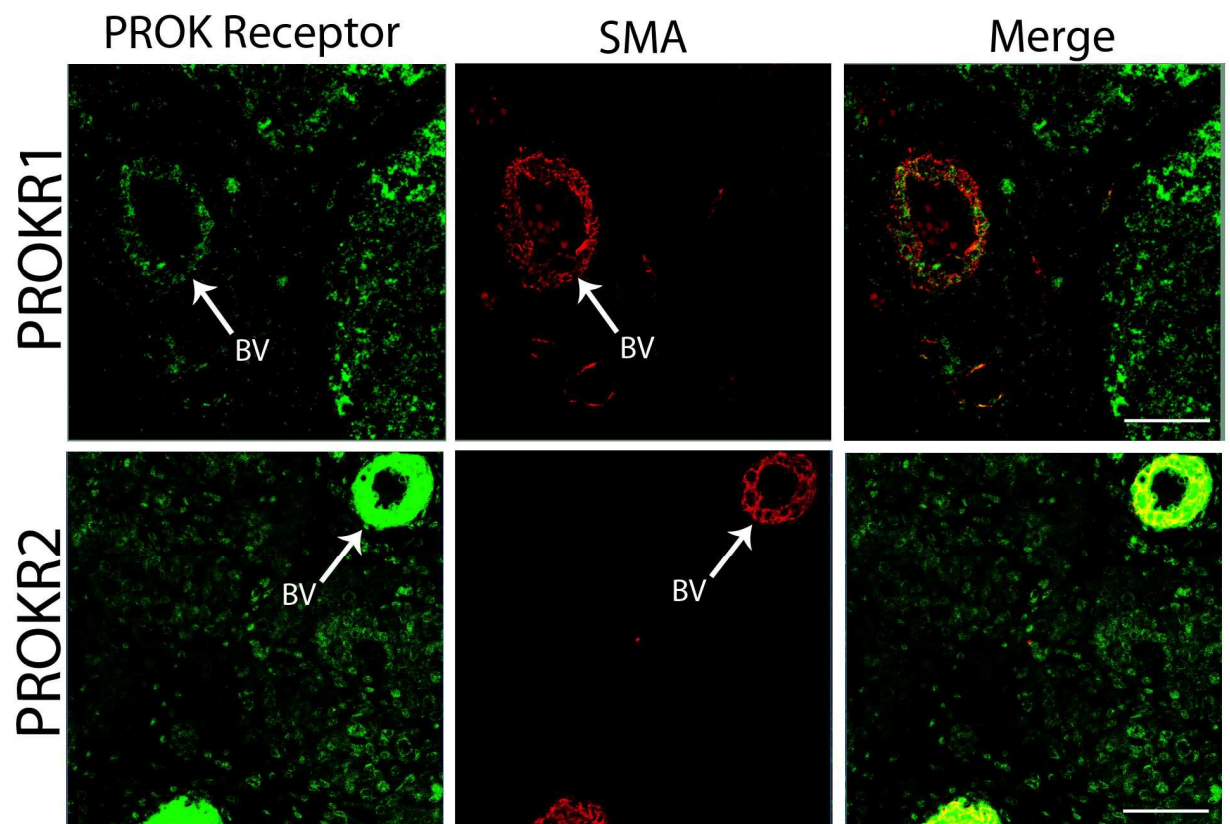


Figure 7.7 *PROK receptors are co-expressed with SMA in fetal testicular vasculature.*

The PROK receptors (green) were co-immunolocalised with the vascular marker α -smooth muscle actin (SMA, red) in human fetal testicular tissue (18 wks). Both (A) PROKR1 and (B) PROKR2 co-localised with SMA in the blood vessels (BV) of the fetal testis. Scale bars equal 50 microns. Images are representative of staining performed on at least three specimens at roughly the same gestation.

7.3.5 PROK1 functions as pro-survival factor in intratubular cells in the human fetal testis

As PROK1 mRNA expression was higher than that of PROK2 and protein expression was also heightened in the human fetal testis compared to the endometrium, where it is known to function, the role of PROK1 was investigated during development in the human fetal testis. PROK1 function was examined via hanging drop culture (as in chapter 3) of fragments of fetal testis (14-17 weeks, n=6) with 40 nM PROK1 or vehicle control for 24 hours. The testis tissue was then examined for histological changes in apoptosis or proliferation as determined by the markers CC3 or BrdU respectively (Figure 7.8 and 7.9). Positively stained cells were quantified and categorised as either extratubular (interstitial) cells or intratubular (within seminiferous tubules), to narrow function to a specific compartment.

As PROK receptor localisation determined the primary site of PROK action was the interstitial compartment of the human fetal testis (both Leydig and non-Leydig cells), the extratubular compartment was postulated to be the main site of PROK1 action. However, upon quantification of apoptosis and proliferation in this compartment, no change in cell apoptosis or proliferation was determined (Figure 7.8).

Apoptosis and proliferation were also quantified in the intratubular (germ and Sertoli cell) population of the human fetal testis. Although no change was seen in proliferation of these cells, there was a significant difference in the rate of apoptosis, with a significant decrease in apoptosis with PROK1 treatment (5.7 ± 4.5 vs $3.6 \pm 2.3 \times 10^{-4}$, $p=0.03$, Figure 7.9). These data suggest PROK1 does not affect the rate of cell turn over in the extratubular compartment which is composed of PROK target cells. However, PROK1 treatment does affect cell turn over in the intratubular compartment suggesting PROK1 signals to the Leydig and/or non-Leydig interstitial cells to produce a paracrine factor that in turn promotes survival in the intratubular compartment consisting of Sertoli and germ cells.

Extratubular Cells

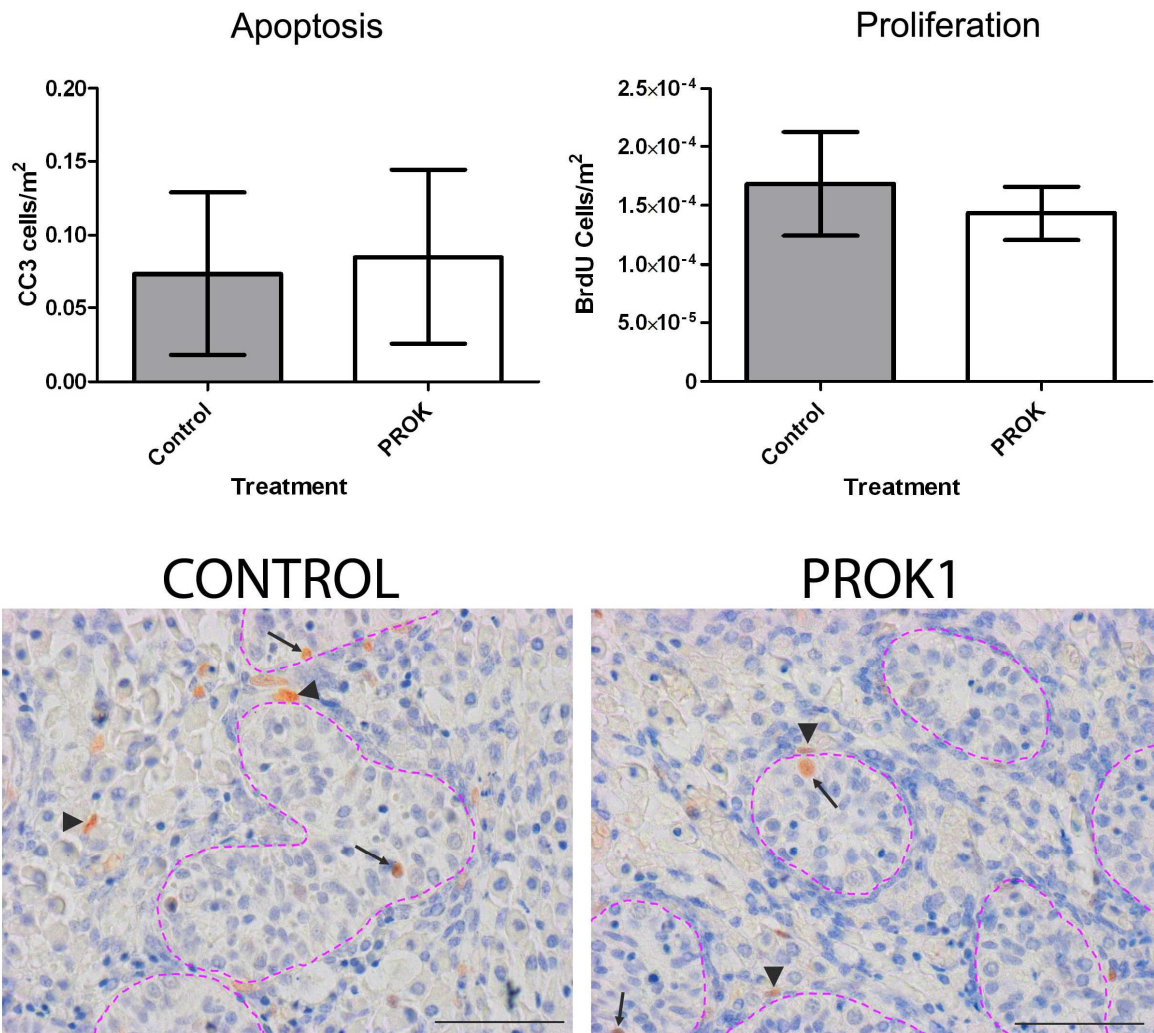


Figure 7.8 *No change in apoptosis or proliferation in the extratubular cells of the human fetal testis with PROK1 treatment*

Apoptosis and proliferation in the extratubular (outwith the seminiferous tubules outlined by dashed line) compartment of the human fetal testis was quantified with the apoptotic marker cleaved caspase-3 (CC3) and the proliferative marker BrdU (14-17 weeks gestation, n=6). Positive cells were quantified and adjusted for extratubular area. This determined PROK1 treatment did not induce a change in cell turnover in the extratubular compartment. Sample BrdU staining from control and PROK1 treated testis, demonstrating no change in extratubular (arrowhead) staining. Intratubular staining marked with arrows. Scale bars equal 100 microns.

Intratubular Cells

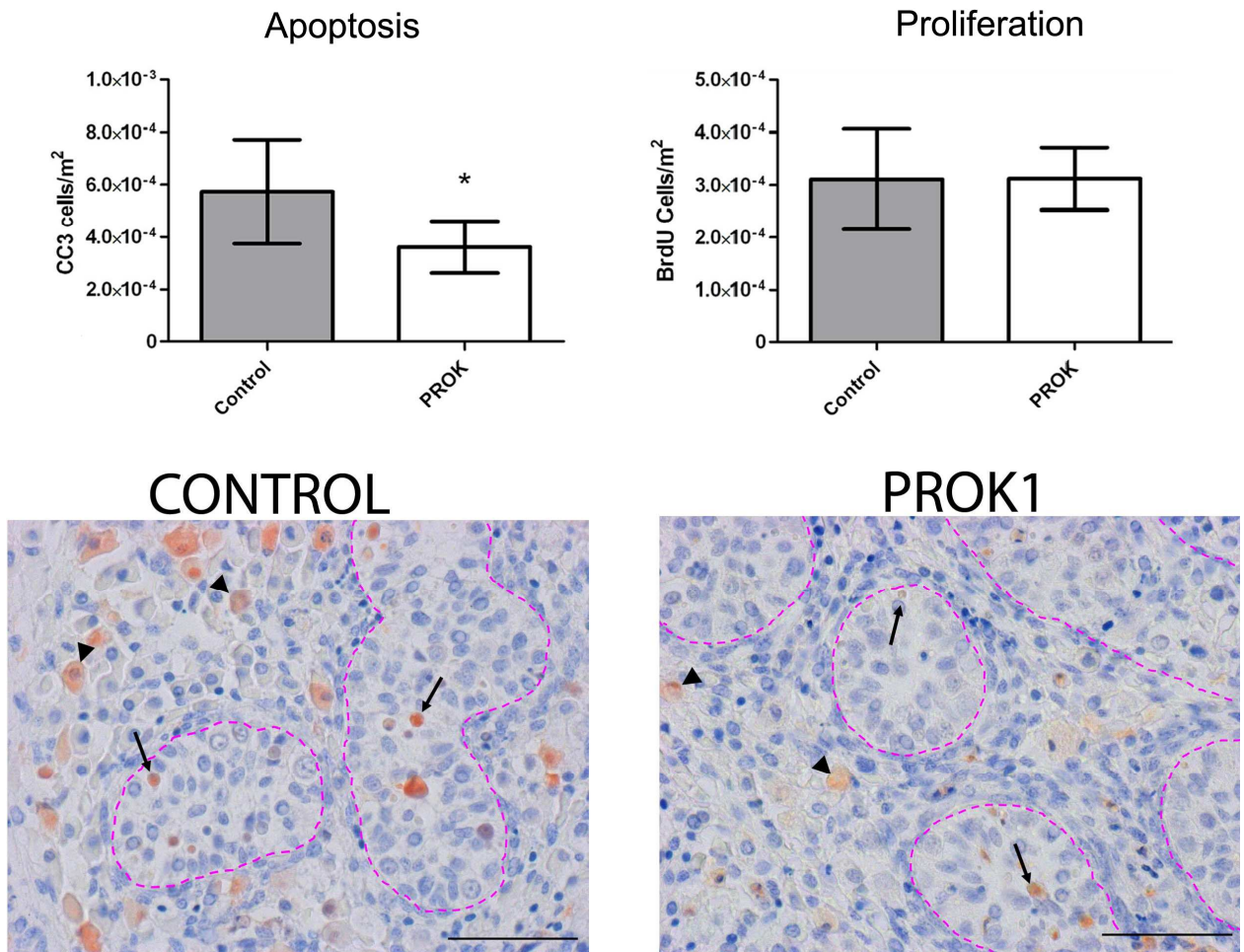


Figure 7.9 Significant reduction of apoptosis in intratubular cells with PROK1 treatment in the human fetal testis

Apoptosis and proliferation in the intratubular compartment (seminiferous tubules outlined by dashed line) of the human fetal testis was quantified with the apoptotic marker cleaved caspase-3 (CC3) and the proliferative marker BrdU (14-17 weeks gestation, n=6). Positive intratubular cells were quantified and adjusted for tubular area. This determined PROK1 treatment significantly reduced apoptosis of intratubular cells (arrows) (*p=0.05) unlike in extratubular cells (arrowheads), but did not alter proliferation rate in either cell type. Scale bars equal 100 microns.

7.3.6 COX2 and DKK1 expression are up-regulated by PROK1 signalling via PROKR1

PROK1 cultures suggest a paracrine downstream factor regulates intratubular cell survival in the human fetal testis. Further investigation was performed to identify possible pathways affected by PROK1 signalling via differential plating of dissociated human fetal testes (n=6, 14-17 weeks gestation), which allowed for the segregation of the interstitial cell complement from the intratubular cells and steroidogenic cells (germ, Sertoli, and Leydig cells do not adhere/survive after dissociation; Figure 7.10). To determine true differential plating was successful, a sample was taken after dissociation of cells and compared to untreated control cells after passage and culture.

A significant loss of germ, Sertoli and Leydig cells after passage was confirmed by significant reduction in cell-specific transcript expression. The germ cell-specific marker *VASA* demonstrated the most significant loss after passage (3.3 ± 1.8 vs $0.1 \pm 0.05 \times 10^{-3}$ relative to *RPL32*, $p=0.0006$), with both the Sertoli cell marker, *AMH* (7.3 ± 2.7 vs $2.0 \pm 1.0 \times 10^{-3}$ relative to *RPL32*, $p=0.02$) and the Leydig cell marker *3 β HSD* also reduced after passage (1.3 ± 0.3 vs $0.2 \pm 0.1 \times 10^{-2}$ relative to *RPL32*, $p=0.02$). There was no change in the non-Leydig interstitial cell marker *Desmin* demonstrating these cells were retained in culture ($p=0.9$). This segregation allowed for further culture and treatment of PROKR1 target cells specifically, rather than the whole testis.

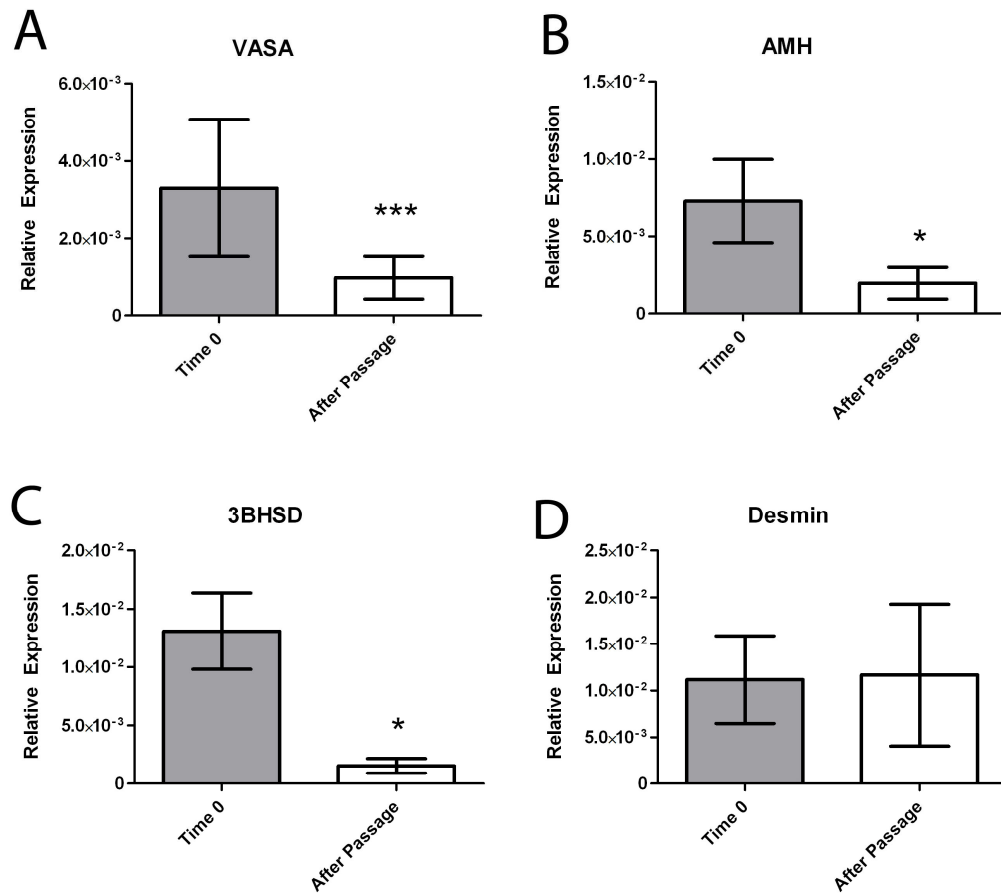


Figure 7.10 Characterisation of the testis interstitial cell cultures

Differential plating of disaggregated fetal testis (n=6, 14-17 weeks gestation) were performed in order to culture PROK specific target cells from the human fetal testis. qRT-PCR analysis of cells before plating and after passage (untreated for 24 hours) was performed to confirm which cell types were sustained. (A) The germ cell gene VASA, (B) Sertoli cell gene AMH and (C) Leydig cell gene 3β HSD were all significantly downregulated post-differential plating determining these cells did not adhere/survive to be PROK1 treated. (D) No change was seen in the interstitial cell marker Desmin demonstrating these cells were able to adhere in culture. * $p \leq 0.05$, *** $p \leq 0.001$.

Several downstream pathways were investigated, including the PG pathway, which has been demonstrated to have pro-survival effects on germ cells in the fetal gonads (ovarian data in chapter 3 and 4, testis data not shown). The PG precursor enzyme *COX2* was significantly up-regulated with PROK1 treatment compared to control (9.7 ± 3.8 vs $3.9 \pm 1.5 \times 10^{-5}$ relative percentage compared to the housekeeping gene *RPL32*, $p=0.05$, Figure 7.11A). However, the PGE₂ specific precursor enzyme PTGES (Figure 7.11B) and known downstream targets of PGE₂ (identified by human fetal cultures in Chapter 3) were not affected (7.11C-D).

Changes in the IL6-type cytokines were also investigated, as it has been postulated they target germ cells and in the endometrium data suggests they are direct targets of PROK1 action (Evans *et al*, 2008; Evans *et al*, 2009). However, no change in expression levels after 24h treatment with PROK1 was identified in *IL6*, *LIF*, *OSM* or *CNTF* (Figure 7.11E-H).

Additionally, the steroidogenic enzymes *CYP11A1* and *StAR* were investigated, as it was postulated PROK1 could be affecting the steroidogenesis pathway either directly or via COX2 regulation, thereby affecting the intratubular cells. However, no change was seen in either target (Figure 7.11I-J).

Finally, two genes identified in an array identifying possible PROK1 targets (Evans, 2008), and known to function in human gonad development were investigated; *DKK1* and *ID3*. *DKK1* was significantly up-regulated with PROK1 treatment compared to control (4.5 ± 1.1 vs $3.6 \pm 1.0 \times 10^{-4}$ relative to *RPL32*, $p=0.03$, Figure 7.11K), but no change was seen in *ID3* (Figure 7.11L).

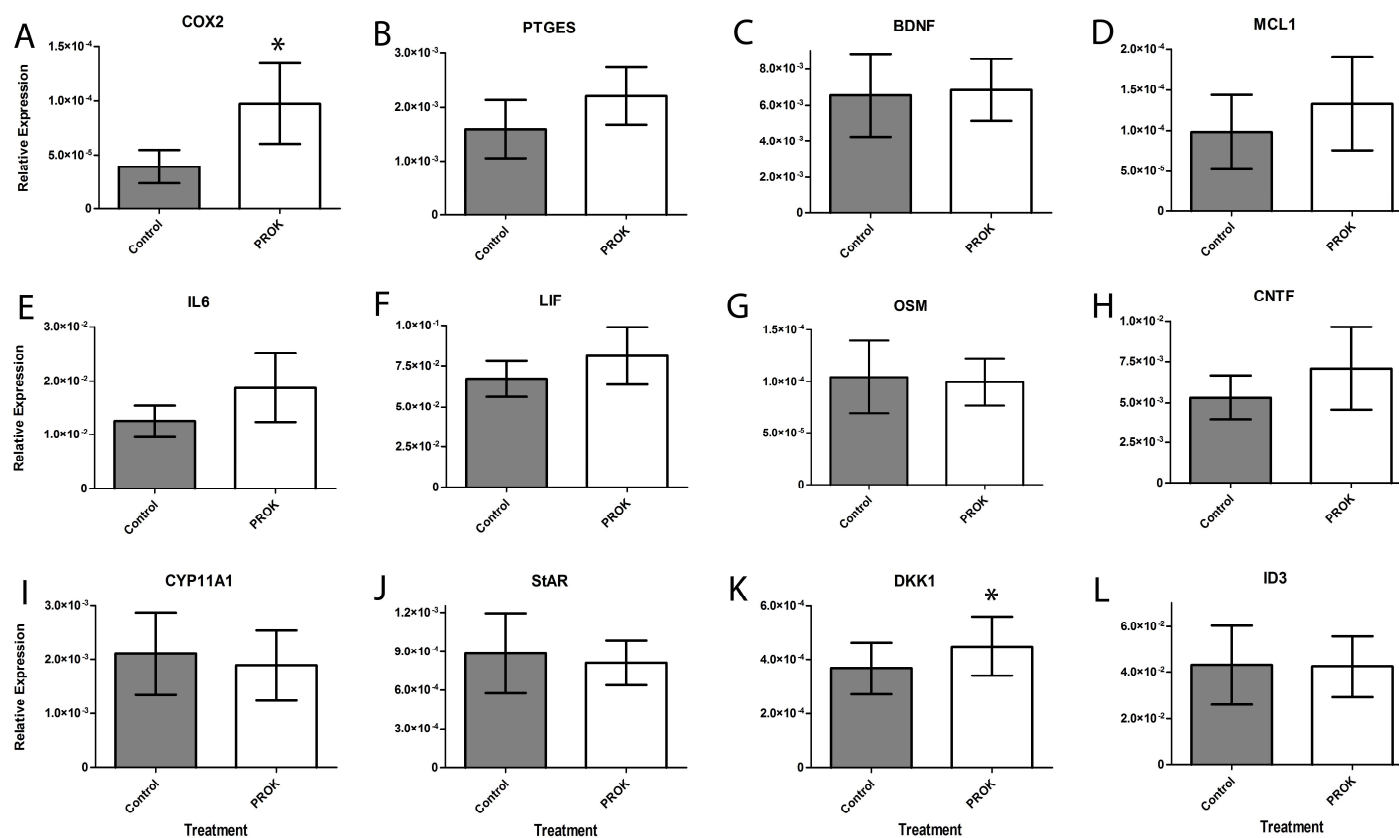


Figure 7.11 Gene expression changes of fetal testis interstitial cells once cultured with PROK1

Interstitial cells collected from human fetal testis samples (14-17 wks) were cultured with 40 nM PROK1 for 24h, resulting in (A) a significant up-regulation of the prostaglandin (PG) pre-cursor enzyme COX2 (*= $p \leq 0.05$) but no change (B) in the PGE₂ specific enzyme PTGES or (C-D) BDNF and MCL-1 known to be regulated by PGE₂. (E-H) No significant change was detected in the IL-6 type cytokines. (I-J) No change was seen in steroidogenic enzymes. (K) Significant up-regulation of DKK1 (*= $p < 0.05$) was detected but no change was seen in ID3 which is known to interact with DKK1 in the fetal gonad. All data are expressed relative to the housekeeping gene *RPL32*. Significance is determined by log transformation (COX2 only) and paired t-test.

7.4 Discussion

As in the ovary, early development of the testis is imperative for adult fertility. The PROK ligands are two recently described proteins involved in angiogenesis and proliferation in other tissues; however despite array data demonstrating that PROK2 expression is high in the fetal testis compared to the ovary (LeCouter *et al*, 2003), PROK function has not been elucidated. This study confirms that PROK ligands and receptors are expressed in the human fetal testis and all components are developmentally-regulated. Additionally, it identifies the interstitial compartment as the site of PROK action in fetal testis, with primary expression of receptors on Leydig and non-Leydig cells as well as vasculature. Notably, this study also identifies a novel function for PROK1 as a pro-survival factor in the fetal testis, in the intratubular cell population consisting of germ and Sertoli cells. Localisation of the PROK receptors suggests this pro-survival effect is due to downstream paracrine signalling. Dissociation and culture of the interstitial cell portion of fetal testes was utilised to determine changes in gene expression and further identify paracrine pathways contributing to increased survival. These cultures identified key components of two pathways which were up-regulated with PROK1 treatment; *COX2* a PG precursor enzyme and *DKK1* an antagonist of the WNT pathway.

As previously demonstrated, inhibition of COX2 via paracetamol exposure leads to germ cell loss in rodent fetal gonads (Chapter 4). Additionally, human fetal ovarian cultures determined that PGE₂ signalling downstream of COX2 is able to up-regulate known differentiation factors (Bayne *et al*, 2009) (Chapter 3). Therefore, up-regulation of *COX2* by PROK1 may account for the pro-survival effects seen. COX2 regulation of steroidogenesis in Leydig cells has also been demonstrated, with inhibition of the enzyme resulting in increased testosterone production (Wang *et al*, 2003b; Wang *et al*, 2005; Chen *et al*, 2007a). Therefore, it was hypothesised that PROK1 regulation of *COX2* might modulate expression of either PGE₂ or steroidogenic components in order to exert pro-survival effects. Factors from both downstream pathways were investigated; however, no significant regulation of either pathway was identified in this study. As these alterations would be secondary to the up-regulation of *COX2* by PROK1 it is possible that subtle changes would not be

detected without additional sample numbers or at later time points. Nevertheless, these data confirm that *COX2* is up-regulated by PROK1 treatment, and that this treatment promotes intratubular survival further supporting the possible role of *COX2* as an anti-apoptotic factor in the fetal gonads.

DKK1 was also up-regulated by PROK1 treatment. *DKK1* (as briefly discussed in Chapter 1) functions in early gonad development by modulating WNT signalling necessary for ovarian development (Vainio *et al*, 1999; Jeays-Ward *et al*, 2003). *DKK1* binds to low-density lipoprotein receptor-related protein 6 (LRP6) a necessary component for WNT signalling (Bafico *et al*, 2001; Mao *et al*, 2001; Semenov *et al*, 2001), making cells less responsive to WNT signalling and preventing activation of downstream β -catenin signalling necessary for ovarian development (Bafico *et al*, 2001; Mao *et al*, 2001; Semenov *et al*, 2001). *Dkk1* is sex-specifically increased in the fetal testis during development (Manuylov *et al*, 2008; Combes *et al*, 2011) and is thought to prevent inappropriate WNT signalling. Loss of Wnt4 signalling using a homozygous null rodent model produced XX gonads with features normally associated with testis development (Yao *et al*, 2004). However, *Dkk1*^{-/-} XY gonads do not show up-regulation of Wnt signalling nor are they feminised (Combes *et al*, 2011) leading to the hypothesis that *Dkk1* plays a supportive role in repression of ovarian development, rather than being a sole protective factor. The fetal testis interstitial culture data support this protective theory, as up-regulation of *DKK1* with PROK1 treatment is concomitant with survival of intratubular cells.

Interestingly, the role for PROK1 in angiogenesis as demonstrated in the adult testis in previous studies (LeCouter *et al*, 2003; Samson *et al*, 2004), was not supported in the fetal testis, as no change was seen in proliferation of the extratubular cell population (including vascular endothelial cells). However, previous angiogenic studies in the testis were performed over 1 week (LeCouter *et al*, 2003). It is possible the cultures utilised in this study did not identify changes in vasculature due to the short period of culture (24h) or due to the stage of testis development, as vascularisation of the testis initiates at the beginning of second trimester with migration of endothelial cells (Nishino *et al*, 2001; Ostrer *et al*, 2007), but would not be as advanced as in later gestations or in the adult.

In addition to functional aspects of PROK1 in the human fetal testis, this study also demonstrates that PROK components are more highly expressed in the human fetal testis than in the ovary at similar gestations (Chapter 6), with developmental increases of PROK signalling components in both sexes, suggesting an increasingly important role for PROK during second trimester in both sexes. The fetal testis is quite dynamic during early development, with several processes occurring simultaneously. Therefore, pinpointing which processes PROK might be involved in based upon expression levels is not possible. However, PROK1 seems to be up-regulated around the initiation of Leydig differentiation and initiation of steroidogenesis (Codesal *et al*, 1990; Murray *et al*, 2000; Gaskell *et al*, 2004); whereas both receptors are up-regulated in late second trimester which is mostly associated with an increase in proliferation, differentiation, and vascular formation (Nishino *et al*, 2001). It is likely, based upon culture and localisation data, that PROK signalling is involved in regulation of some of these processes.

In addition to differential transcript expression between the sexes, there is also a discrepancy in PROK protein localisation. PROK targets the germ cells in the human fetal ovary, whereas in the testis the interstitial compartment is the site of PROK action. The two PROK receptors also display a striking difference in localisation, with PROKR1 primarily expressed in the non-Leydig interstitial cells and PROKR2 expressed by the Leydig cells. Although both receptors were expressed by the testicular vasculature, this drastic difference in primary site of localisation suggests the two receptors play differing roles during testis development. As PROK1 is able to signal interchangeably via either PROK receptor, it is not known which receptor is responsible for demonstrated pro-survival effects.

Regulation of *COX2* and *DKK1* in cell lines transfected with the PROKR1 gene (Chapter 6) (Evans *et al*, 2008; Evans *et al*, 2009; Macdonald *et al*, 2010) support this mechanism for regulation in the testis. However, PROK1 treatment of PROKR1 transfected cells has a negative effect on proliferation in an endometrial epithelial cell line *in vitro* (Macdonald *et al*, 2010). Further investigation utilising receptor-specific antagonists would be beneficial for dissecting specific roles for PROKR1 and 2 in the fetal testis.

In conclusion, these data demonstrate that PROK ligands and receptor transcripts are developmentally-up-regulated and are expressed at higher levels in the human fetal testis than ovary. Additionally, in the fetal testis PROKs primarily target the Leydig and non-Leydig interstitial cells with additional expression in the vasculature.

Despite this localisation, it was determined that PROK1 was able to promote survival of intratubular cells, inferring paracrine signalling to these cells, which may be via *DKK1*, *COX2*, or another downstream target yet to be identified. These data outline a novel role for PROK function in the human fetal testis and demonstrate it functions as a pro-survival factor during development.

Chapter 8

General Discussion

Chapter 8. General Discussion

8.1 Introduction

Fetal ovarian development encompasses several highly regulated events, from initial germ cell specification and migration to the proximal epiblast in formation the gonad, followed by sex determination, entry into meiosis and subsequent arrest, and concluding in germ cell nest breakdown and association of oocytes with granulosa cells to form primordial follicles. In addition to these developmental processes, germ cell number is also highly regulated across fetal ovarian development, the few germ cells generated at initial specification proliferate vastly, only for their number to be drastically reduced prior to primordial follicle formation. The regulation of both germ cell survival and development leads to the establishment of a primordial follicle pool, which defines the number of oocytes a woman will have for ovulation in adulthood, and thus determine her future fertility. Regulation of germ cell differentiation is provided by autocrine, paracrine, and juxtacrine signalling from both the germ cells themselves and their somatic environment, collectively termed the germ cell niche. Although identified as such, the factors which comprise the germ cell niche remain to be fully elucidated. This thesis encapsulates several studies that aimed to identify novel regulators of ovarian development, in an effort to further clarify what governs germ cell development and survival.

Three signalling pathways were initially hypothesised to regulate human fetal ovarian development, and thereby be part of the germ cell niche: prostaglandins (and specifically PGE₂), IL6-type cytokines, and the PROKs. These postulated regulators were identified as germ cell niche candidates for several key reasons (interaction with established factors of the germ cell niche, regulation of the adult ovary, and/or differentially regulated during early ovarian development) and were further investigated in order to establish the role of each factor, how they interact with established factors of the germ cell niche, and other postulated regulators.

8.2 Novel interactions in the germ cell niche

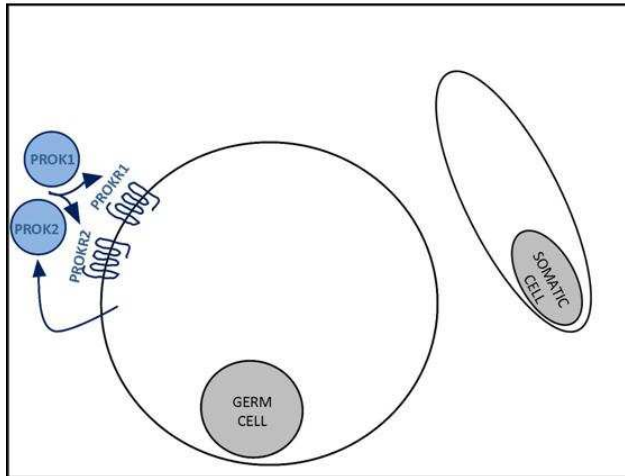
The experimental studies which constitute this thesis have demonstrated several novel factors and mechanisms within the germ cell niche (summarised in blue in Figure 8.4). These data provide further understanding of the inter-relationships between factors involved in germ cell development, as well as providing additional hypotheses for further interaction.

These data demonstrated that PROK1 and PROK2 signal in an autocrine manner to both PROKR1 and R2 receptors which are solely expressed by germ cells in the human fetal ovary (Figure 8.1A). Further, PROK1 via PROKR1 is able to up-regulate *COX2* expression (Chapter 6, Figure 8.1B), thereby demonstrating interaction between two of the postulated pathways.

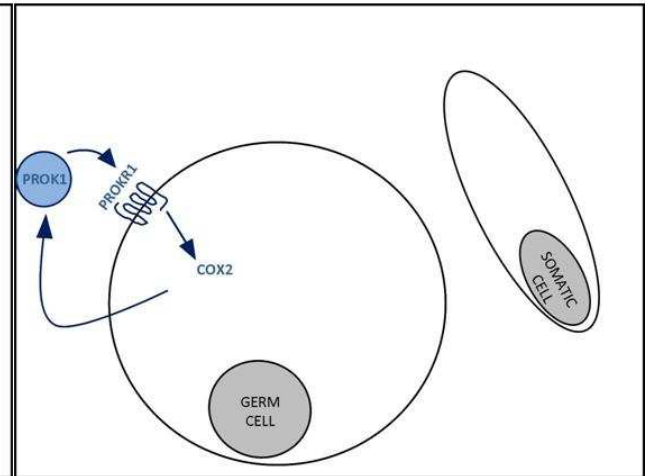
Outwith the characterisation of novel components of the germ cell niche in the ovary, the work included in this thesis has also identified differential roles for the PROKs in the human fetal testis (as compared to the ovary, Chapter 7). These studies identified that not unlike in the ovary, PROK1 via PROKR1 is able to up-regulate *COX2* and promote survival of cells (Figure 8.1D). However, unlike the ovarian studies, PROK ligands were shown to solely target interstitial cells in the human fetal testis (Leydig and non-Leydig) and act in a paracrine fashion affecting intratubular cells rather than in an autocrine manner (Figure 8.1C). It was further demonstrated PROK1 is also able to regulate *DKK1*, a factor involved in sex determination, and thus may further promote survival via a male-specific pathway. As in the ovary, it is postulated PROK1 via PROKR1 up-regulation of *COX2* may be protective via interaction with the steroidogenesis pathway, whereby COX2 increases testosterone production promoting intratubular survival.

Human Fetal Ovary

A) Signalling

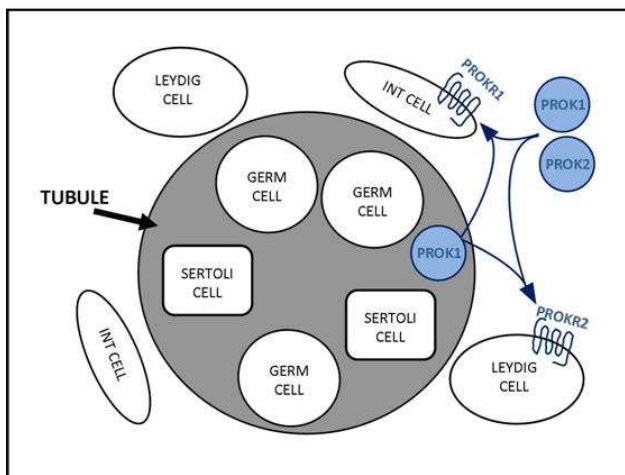


B) Downstream Regulation



Human Fetal Testis

C) Signalling



D) Downstream Regulation

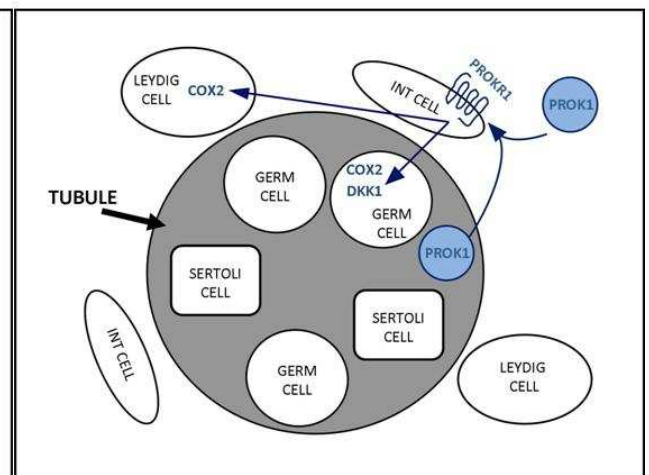


Figure 8.1 Prokineticin signalling in the fetal gonads

Summary of PROK signalling differences in the human fetal gonads as determined by studies in this thesis. A) In the ovary the PROK ligands are expressed by the germ cells as are the PROK receptors demonstrating an autocrine signalling mechanism, B) with further data demonstrating PROK1 via the PROKR1 receptor is able to regulate COX2 in the germ cells. C) Conversely, in the fetal testis ligand expression is more diffuse and the PROK receptors are localised to interstitial cells. D) However, as in the ovary, PROK1 via PROKR1 is able to regulate COX2 expression as well as DKK1, a factor involved in sex-determination, both of which are expressed in other cells demonstrating paracrine downstream signalling. (Abbreviations: INT-interstitial, TUBULE- seminiferous tubule).

However, it is unlikely that all of the COX2 produced in the fetal ovary is a direct result of PROK1 signalling, as *COX2* expression increases linearly with gestation; whereas *PROK1* up-regulation is later in late second trimester. Further, it is possible that signalling by PROK2 via the same receptor (PROKR1) may have an additive effect; as PROK signalling has the potential for redundancy. In addition, *PROK2* unlike *PROK1* displays a similar pattern of expression to that of *COX2* in the ovary. Despite the possibility of an additive effect of PROK signalling, it is unlikely this is the only regulatory pathway up-stream of COX2 production in the ovary. Data from mice homozygous null for *PROKR1* and *PROKR2* support this hypothesis, as neither demonstrate any alteration in ovarian function ((Negri *et al*, 2006; Matsumoto *et al*, 2006) unlike *COX2*^{-/-} and *EP2*^{-/-} females, which are unable to ovulate normally (Dinchuk *et al*, 1995; Hizaki *et al*, 1999)). These data suggest further regulators outwith the PROKs, are responsible for some of the COX2 production in the human fetal gonads, particularly in earlier gestation (14-16 weeks), at which time *COX2* expression is up-regulated but *PROK1* expression is not.

Following up-regulation via PROK1 and other possible pathways, COX2 and subsequently, PTGES synthesize and release PGE₂ from fetal germ cells in the human fetal ovary, which then acts in an autocrine (via receptors EP2, 3, or 4, Figure 8.2A) or paracrine fashion (via EP3 or 4, Figure 8.2B) in order to regulate downstream targets including Activin A (*INHBA*), *BDNF*, and *MCL-1* (Chapter 3, Figure 8.2C).

It is hypothesised that regulation of Activin A is downstream of PGE₂ signalling via the EP2 receptor (Figure 8.2C), as this receptor is solely expressed by more mature germ cells, which are the site of Activin A expression and regulation, whereas EP3 and 4 are expressed by both somatic and germ cells. It therefore appears that PGE₂ promotes the role of Activin A in germ cell survival and proliferation (Martins da Silva *et al*, 2004). Further, data from this thesis suggest that PGE₂ promotes the inhibition of membrane-bound KL via increased expression of Activin A, which was previously demonstrated in the human ovary (Childs *et al*, 2010a), thereby preventing precocious primordial follicle formation.

BDNF expression is also stimulated by PGE_2 in the human fetal ovary, and may do so via two pathways. As the PGE_2 receptors EP3 and EP4 are expressed by somatic cells, the site of *BDNF* expression, PGE_2 may directly up-regulate expression of *BDNF* in the somatic cells (Figure 8.2C). However, previous data have suggested a second mechanism, as *BDNF* is known to be regulated by Activin A in the human fetal ovary (Childs *et al*, 2010a) suggesting regulation may be via an indirect mechanism rather than via direct PGE_2 action (Figure 8.2D). Further, it is possible both mechanisms are functional in the regulation of *BDNF* expression. In this regard, it would be beneficial to perform interstitial-only ovarian cultures and compare with whole ovarian cultures to determine the route of regulation. However, as prostaglandins were initially identified as regulators of the neurotrophins in the endometrium (Jabbour, unpublished), a tissue which lacks a germ cell component, it is likely *BDNF* is up-regulated directly via PGE_2 signalling to the somatic cells or via additive direct and indirect signalling. Regardless of the initial mechanism, *BDNF* is then able signal via the TrkB receptor, which is known to be essential for oocyte survival at this time (Spears *et al*, 2003; Kerr *et al*, 2009).

Data from this study has also identified PGE_2 regulation of the anti-apoptotic factor MCL-1. As with *BDNF*, increased expression of *MCL-1* is postulated to be either direct via PGE_2 regulation (Figure 8.2C) or indirect (Figure 8.2D) downstream of regulation via Activin A (Hartley *et al*, 2002; Martins da Silva *et al*, 2004). Data from lung adenocarcinoma cultures also demonstrate MCL-1 regulation downstream of COX2 signalling is a pathway that is conserved in several tissues (Lin *et al*, 2001; Chen *et al*, 2010). Activation of this pathway further supports the hypothesis that PGE_2 acts as a pro-survival factor during human fetal ovarian development, a hypothesis that was supported by studies inhibiting COX2 expression (and thereby PGE_2 production) in fetal rat ovaries *in vivo* (Chapter 4). However, this thesis has demonstrated fetal COX2 inhibition lead to significant oocyte loss that was not via increased apoptosis or decreased proliferation. It is hypothesised that part of this phenotype may be the result of decreased Activin A, *BDNF* and MCL-1 production via inhibition of PGE_2 signalling, and that this signalling in turn may have some effect on maturation/development of germ cells, instead of affecting apoptosis.

However, an alternative hypothesis is that the reduction in germ cell number is a result of COX2 regulation of steroidogenesis (Figure 8.2E), which has been demonstrated in adult tissue (Wang *et al*, 2003b; Wang *et al*, 2005; Chen *et al*, 2007a). Testosterone production is indeed perturbed in the male counterparts exposed to COX2 inhibition in this study. Therefore, it is suggested the loss of oocytes might be due to altered steroidogenesis in the ovary. Although little is known about the role of steroid regulation in the human fetal ovary, estrogen has been established as a key factor necessary for germ cell nest breakdown in the mouse thereby allowing for primordial follicle formation (Iguchi *et al*, 1986; Kezele & Skinner, 2003; Chen *et al*, 2009). If steroidogenesis is altered by COX2 inhibition, thereby reducing testosterone or if indeed estrogen is directly affected by COX2 inhibition, it is possible germ cell nests are precociously broken down, resulting in germ cell atresia out-with programmed cell death. It is also possible that alteration of testosterone alone could affect germ cell survival, as ARKO female mice undergo early ovarian failure (Shiina *et al*, 2006).

Further, data from a non-human primate model suggests a similar role for estrogen (Zachos *et al*, 2002) and has determined that estrogen may regulate germ cell nest breakdown via up-regulation of microvilli expression, ECM proteins, and altering the Activin : Inhibin ratio (Billiar *et al*, 2003; Billiar *et al*, 2004; Zachos *et al*, 2004; Bocca *et al*, 2008; Zachos *et al*, 2008). These data suggest a similar mechanism is also likely in the human, where expression of steroid receptors and synthesis enzymes have been confirmed (Fowler *et al*, 2011).

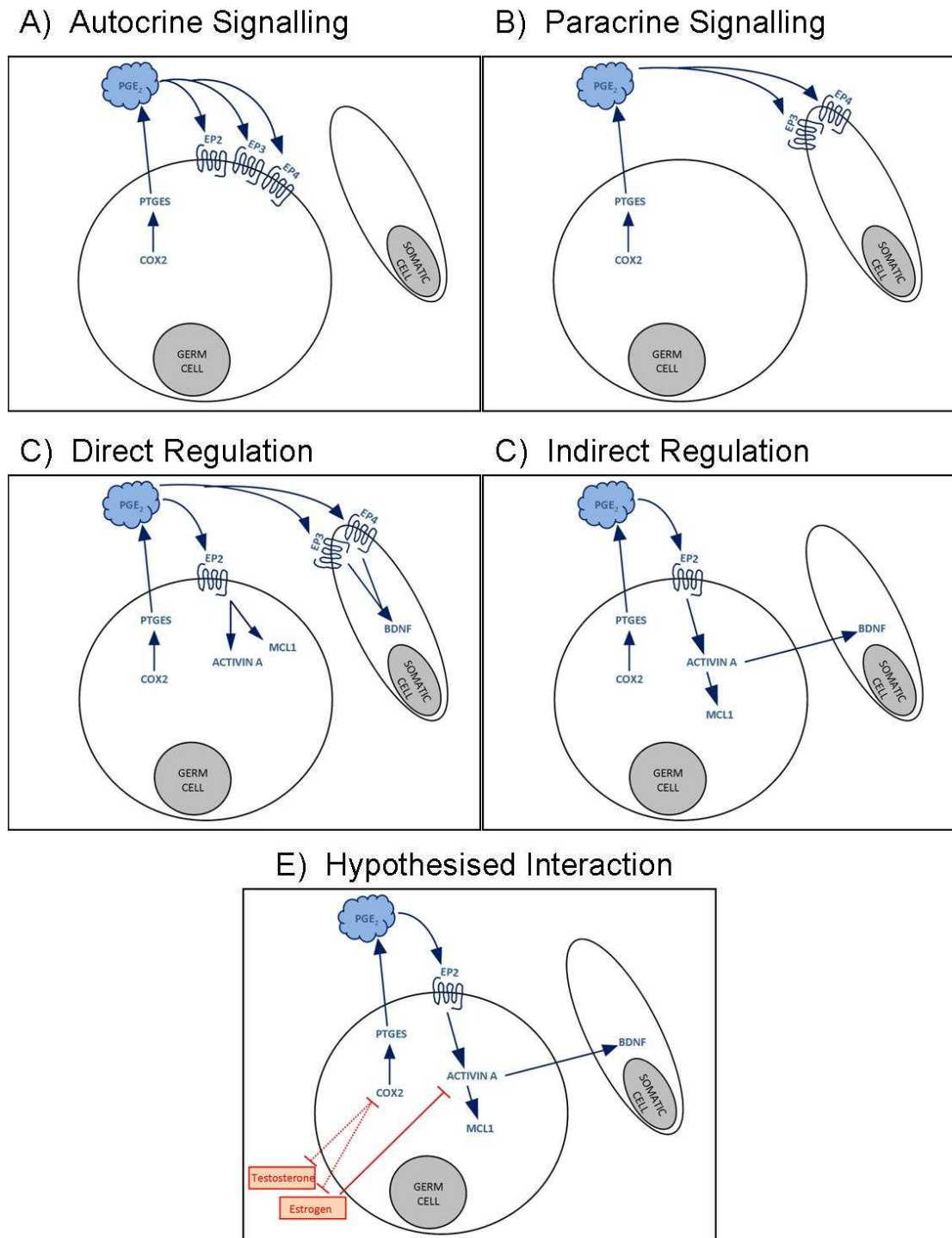


Figure 8.2 Prostaglandin signalling in the fetal ovary

Data from this thesis has determined that PGE_2 is able to signal in both an A) autocrine and B) paracrine manner, with downstream up-regulation of Activin A, MCL1 and BDNF, which maybe via either C) direct or D) indirect mechanisms. In addition, it is hypothesised that this pathway might also interact with the steroid hormone pathway to further regulate human ovarian development.

Another further group of factors has further been characterised in the human fetal ovary, the IL6-type cytokines (Chapter 5). Although function of these factors has not been investigated in this thesis, the present data demonstrate that they solely target germ cells in the human fetal ovary, as their shared receptor components gp130 and LIFR are exclusively localised to these cells (Figure 8.3A). Investigation of the IL6-type cytokines has further demonstrated developmentally-regulated transcript expression of the shared receptor components and the OSM ligand in the period leading up to primordial follicle formation. Based on these data, it is hypothesised that the IL6-type cytokines are likely to function in later oocyte development. As LIF has previously been shown to regulate the primordial to primary transition in the rodent ovarian culture, it may play a similar role in the human (Nilsson *et al*, 2002; Nilsson & Skinner, 2004). Both KL and bFGF, which are well-established in cooperation with LIF in the maintenance of stem cell culture, also function alongside LIF to promote follicle activation in these rodent ovarian cultures. In addition, similar up-regulation of *bFGF* and *KL* (as compared to the IL6-type receptors) is noted in the human (Figure 8.3B) (Robinson *et al*, 2001; Quennell *et al*, 2004; Stoop *et al*, 2005) suggesting a mechanism of bFGF/LIF/KL interaction may be important in the human as well as in the rodent for follicle transition, however this remains speculative. Further study of IL6-type cytokine interaction with bFGF and KL, as well other established regulators of follicle activation including FOXO3a, GDF9 and BMP15, would further clarify the roles of these factors in the human fetal ovary.

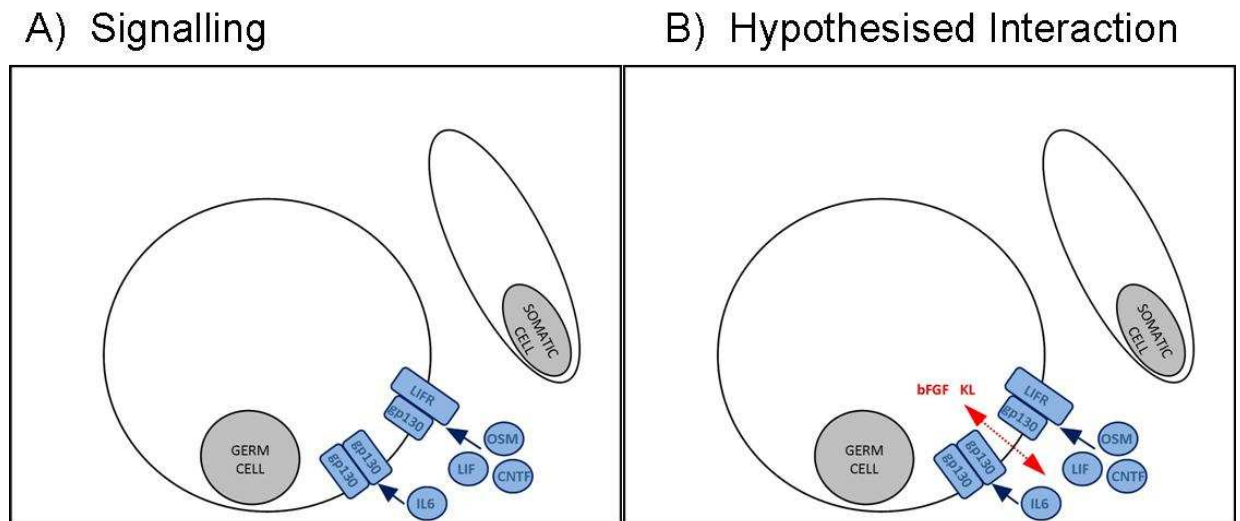


Figure 8.3 *IL6-type cytokine signalling in the fetal ovary*

This thesis has determined A) the IL6-type cytokines signal solely to the germ cells in the human fetal ovary as their two shared receptors (gp130 and LIFR), necessary for all IL6-type signalling, are located on these cells. In addition, mRNA expression patterns suggest the IL6-type cytokines may play a role in later follicular development, B) leading to the hypothesis that the IL6-type cytokines may interact with bFGF and KL, which are important for later germ cell development *in vivo* and are known to interact with the IL6-type cytokine *in vitro*.

8.3 Conclusions

In conclusion, this thesis has demonstrated PGE₂, the IL6-type cytokines, and the PROKs are all expressed in the human fetal ovary, and signal directly to the germ cells (summarised in Figure 8.4). Additionally, functional studies have identified PROK1 and PGE₂ are up-stream of pro-survival and proliferation pathways and thereby play a role in regulating fetal oocyte development as part of the germ cell niche. PROK1 also plays a similar pro-survival role in the fetal testis. However, in both the fetal testis and the fetal ovary, it is likely that COX2 downstream of PROK1 plays a larger role pro-survival/anti-apoptotic function, as COX2 is able to directly modulate these pathways via several downstream targets including Activin A, BDNF, and MCL-1, as well as a likely link with steroidogenesis. In addition, this thesis further speculates that the COX2 produced by the fetal ovary is not solely the result of increased PROK1 signalling, and that other up-stream regulatory pathways have yet to be identified.

These studies have contributed to the understanding of fetal ovarian development in the human, and as such have provided further knowledge regarding what factors influence germ cell death and survival prior to primordial follicle formation. Disruption of these developmental events can result in POI or infertility, and thus understanding these pathways is essential for women's reproductive health.

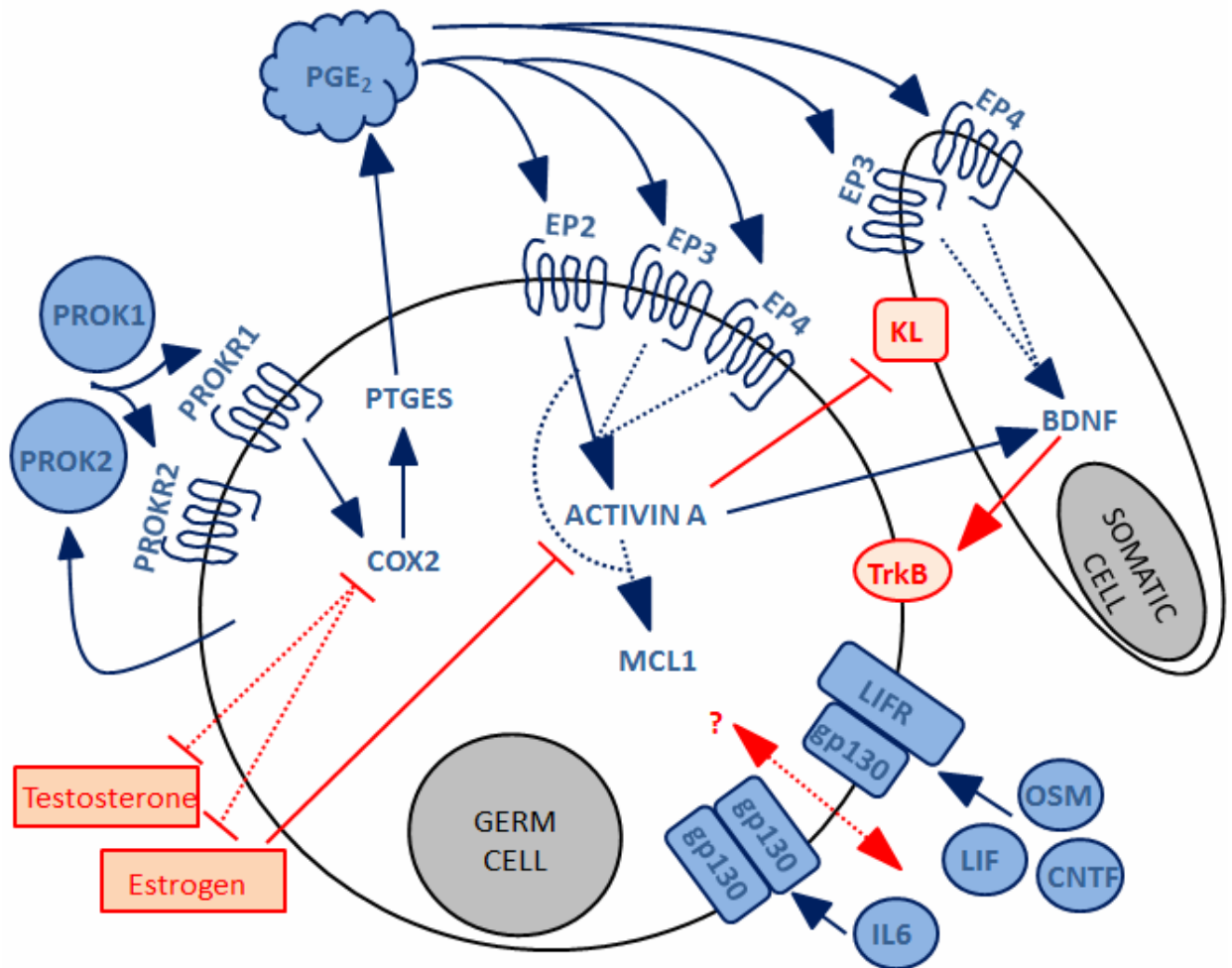


Figure 8.4 *Summary of the novel pathways involved in the germ cell niche and their likely interactions with established pathways*

Schematic representation of the newly characterised factors of the germ cell niche and their downstream interactions (blue), in corporation with suggested interactions with established signalling pathways essential for early germ cell survival and development (red). Established pathways are demonstrated in solid lines whereas those hypothesised are represented by dashed lines. In the case of EP2 regulation of Activin A, this pathway is not established, but is most likely.

8.4 Future Work

Although this thesis initially established function for novel factors in the human fetal ovary and testis, further work is necessary to fully understand the mechanisms and overall function of these factors throughout ovarian biology. Follow-up studies of particular importance are as follows:

8.4.1 Paracetamol Exposure Study

The paracetamol study is of particular interest for further work, as data from e17.5 rats has demonstrated there is no change in germ cell number in early gestation, and there is no apparent mechanism for loss by e21.5 (no change in apoptosis or proliferation). Therefore, further analysis of ovaries at this stage is necessary in order to establish possible mechanisms of action. Data from the male paracetamol exposed pups has noted a change in steroidogenesis, suggesting it will be important to investigate levels of steroid expression in the female pups, as well as levels of PGE₂ to identify the likely downstream targets of paracetamol action resulting in reduced germ cell number. To that end, the levels of steroids and PGE₂ will also be investigated in the dam to see how the maternal system is affected. As discussed previously, estrogen is known to function in nest breakdown and alteration of the estrogen levels in the dam could possibly perturb this process in the pups.

In addition, as a reduction in germ cell number is likely to impact on primordial follicle formation and thus affect adult fertility, future studies are planned to track effects of paracetamol exposure on primordial follicle formation in offspring, and throughout postnatal life in order to identify possible premature follicle depletion in aged paracetamol-exposed females.

8.4.2 PROK1 effects in the human fetal testis

Although it was determined that PROK1 functions to reduce apoptosis in intratubular cells of the human fetal testis, further study is necessary to determine if this increased survival is of Sertoli or germ cells (or both). Identification of which cell type is being affected will aid in understanding downstream mechanism of PROK action, and will be performed by stereological analysis of dual detection for a germ cell marker and cleaved caspase-3.

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Appendix 1: Manufacturers' Details:

Company	City	Country
Abcam	Cambridge	UK
Adobe	San Jose, CA	USA
Ambion	Austin, TX	USA
Applied Biosystems	Foster City, CA	USA
BD	Franklin Lakes, NJ	USA
Bioline	London	UK
Bio-Rad	Hercules, CA	USA
Biotium	Hayward, CA	USA
Caltag	Buckingham	UK
Cayman	Ann Arbor, MI	USA
Clintech	Guilford	UK
Corning	Corning, NY	USA
CoStar	Schipol-Rijk	Netherlands
Dako	Glostrup	Denmark
Eppendorf	Hamburg	Germany
Eurogentec	Liege	Belgium
Faithfull Tools	Kent	UK
Fisher Scientific	Loughborough	UK
Fitzgerald	Acton, MA	USA
Gibco	Carlsbad, CA	USA
GraphPad Software	La Jolla, CA	USA
Histolab	Gotheburg	Sweden
Invitrogen	Carlsbad, CA	USA
Invivogen	San Diego, CA	USA
Lab Vision Corp	Now owned by Thermo Scientific (see below)	
Labsystems	Vienna, VA	USA
Leica	Wetzlar	Germany
Li-Cor	Lincoln, NE	USA
Lifespan	Seattle, WA	USA
Lonza	Basel	Switzerland
Lymphotec	Tokyo	Japan
Mazola	Memphis, TN	USA
MBL	Woburn, MA	USA
Media Cybernetics	Bethesda, MD	USA
Millipore	Billerica, MA	USA
Mirus	Madison, WI	USA
MJ Research	Waltham, MA	USA
New England Biolabs	Ipswich, MA	USA
Olympus	Essex	UK
Qiagen	Hamburg	Germany
Qimaging	Surrey	Canada
Perkin Elmer	Waltham, MA	USA
Phoneix	Burlingham, CA	USA
Prior	Cambridge	UK
Promega	Madison, WI	USA
Roche	Basel	Switzerland

Company	City	Country
Santa Cruz	Santa Cruz, CA	USA
SDS	Dundee	UK
Sigma	St Louis, MO	USA
SPPS	Argenteuil	France
Thermo Scientific	Waltham, MA	USA
Upstate	Now owned by Millipore (see above)	
Vector	Burlingame, CA	USA
VWR	West Chester, PA	USA
Zeiss	Oberkochen	Germany

Appendix 2: Publications relating to this thesis